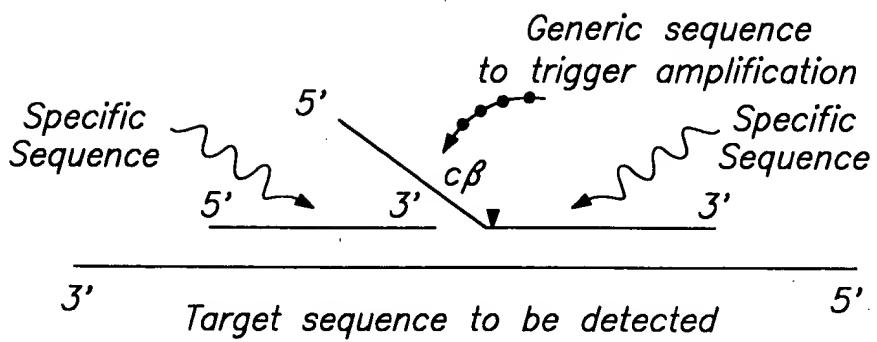
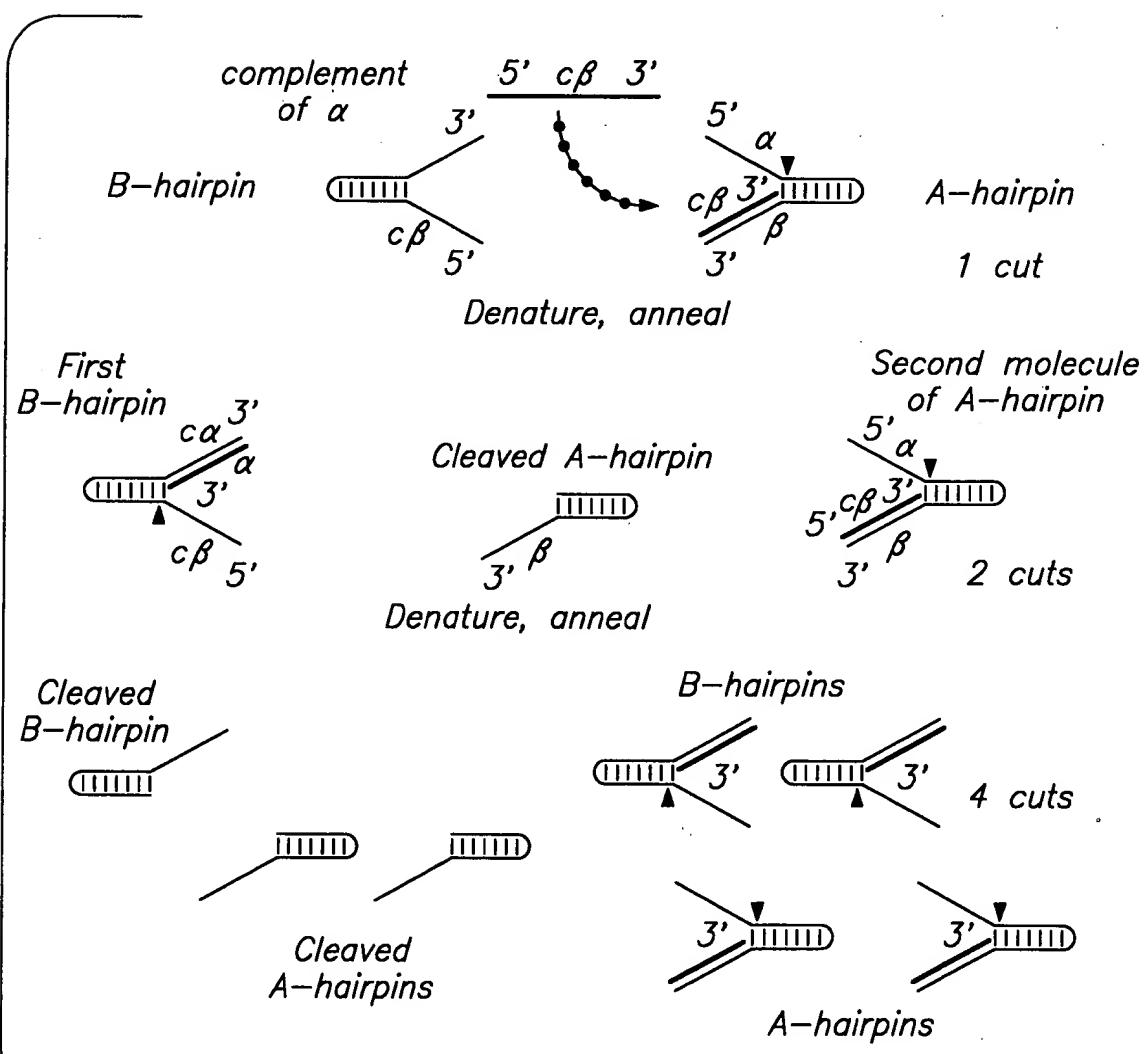


**FIG. 1A**

**FIG. 1B**



**PART ONE: TRIGGER REACTION**



**PART TWO: DETECTION REACTION** —

FIG. 2A

FIG. 2B

MAJORITY	[SEQ ID NO:7]	CGAGGGGAGGAGCTXGTGCCACCTGGCAAAGGGAAAGGAGGGTACGAGGTGGCATCCTC
DNAPTAQ	[SEQ ID NO:1]	C.....G.....G.....G.....C.....C.....C.....C..... 417
DNAPTFL	[SEQ ID NO:2]	T.....G.....G.....G.....G.....G.....G.....G..... 414
DNAPTR	[SEQ ID NO:3]	T.....G.....G.....G.....G.....G.....G.....G..... 420
MAJORITY		ACGGGGACCCGACCTTACGACCTTCCGACCCATGGCGCTCCACCGAGGGTACCTCA
DNAPTAQ		.....AAA.....T.....G.....G.....G.....A.....G.....A..... 487
DNAPTFL		.....T.....A.....G.....C.....G.....A.....T.....G..... 484
DNAPTR		.....A.....G.....C.....G.....A.....G.....G.....G..... 490
MAJORITY		TGACCCGGCTGGCTTGGAGAAGTACGGCTGAGGGGAGCACTGGTGGACTACGGGCGCTGGC
DNAPTAQ		.....G.....A.....A.....G.....G.....G.....G.....G..... 557
DNAPTFL		.....A.....AC.....C.....C.....C.....A.....G..... 554
DNAPTR		.....A.....G.....C.....T.....G.....C.....C.....T..... 560
MAJORITY		GGGGACCCCTGGACACCTCCCCGGCTAAGGGATGGGAGAACACCCCCXGAAGCTCCTCXAG
DNAPTAQ	C.....GAG.....T.....G.....G.....G.....G.....A..... 627	
DNAPTFL	.....G.....T.....A.....G.....G.....A.....G.....A..... 624	
DNAPTR	.....A.....G.....A.....G.....T.....G.....A..... 630	
MAJORITY		GAGTGGGGAGCTGGAAACCTCTAAGAACCTGGACCCGTGAAGGGCGC...CXTCCGGAGAAGA
DNAPTAQ		.....GG.....G.....A.....A.....A.....A.....A..... 694
DNAPTFL		.....T.....G.....G.....A.....T.....T.....G.....G..... 691
DNAPTR		.....A.....A.....A.....A.....A.....A.....A..... 700

FIG. 20

**FIG. 2D**

MAJORITY	CCCGCATGGCTCCCTACCTCTGGACCCCTCCACACCCACCCCCGAGGGGTGGCGGGGCTACGG
DNAPTAQ	[SEQ ID NO:1] ..... G. T. ..... A. ..... AG. ..... C. ..... A. ..... T. G. ..... CC. ..... C. ..... C. ..... 1114
DNAPFL	[SEQ ID NO:2] ..... AA. ..... G. ..... G. ..... C. ..... G. ..... T. G. ..... A. A. ..... T. G. ..... 1111
DNAPTR	[SEQ ID NO:3] ..... C. ..... C. ..... C. ..... C. ..... C. ..... T. C. ..... G. A. ..... G. ..... 1120
MAJORITY	GGGGGACTGGACGGAGGAAGGGGGAGGGGGCGCTCTGGAGAGGCTCTTCCXGAACCTXXXGGAG
DNAPTAQ	C. ..... G. ..... G. ..... GC. ..... T. ..... GC. ..... GTG. ..... G. ..... 1254
DNAPFL	..... T. ..... A. ..... GG. ..... C. C. ..... A. C. ..... AAA. ..... 1251
DNAPTR	..... C. ..... G. CCC. G. ..... G. G. ..... CAT. G. ..... CCTA. ..... 1260
MAJORITY	CGCTTGGGGGAGGAGGGCTCTGGCTTACCAAGAGCTGGAGAACCCCTTGGGGGCTCTGG
DNAPTAQ	A. G. ..... A. ..... A. ..... AC. C. ..... G. ..... G. ..... GCT. ..... G. ..... 1324
DNAPFL	..... A. ..... A. ..... A. ..... G. ..... G. ..... G. ..... GT. ..... 1321
DNAPTR	..... G. ..... A. ..... C. ..... C. ..... A. ..... C. ..... 1330
MAJORITY	CCGACATGGGGGAGGGGTAGGGCTGGACGTGGCTACCTCCAGCCCTXCTGGAGGTGGCGA
DNAPTAQ	..... G. ..... C. ..... T. ..... AG. ..... T. G. ..... G. ..... 1394
DNAPFL	..... GG. ..... G. ..... G. ..... G. ..... G. ..... A. C. ..... 1391
DNAPTR	..... C. ..... A. ..... T. ..... T. ..... C. T. ..... 1400

FIG. 2E

MAJORITY	[SEQ ID NO:7]	GGAGAGTCCCCCTGGAGGAGCTTCCCCCTGGGGACCCCTGAACTCAACTGGGGAC	
DNAPTAQ	[SEQ ID NO:1]	.....GC.....CC.....	1464
DNAPTFI	[SEQ ID NO:2]	.....G.G.....AG.....G.....	1461
DNAPTR	[SEQ ID NO:3]	.....T.....G.....	1470
MAJORITY		CAGCTGAAAGGGTCTTACGGAGCTXGGCTTCCCCCATGGCAAGGGAGAGACXGGCAAC	
DNAPTAQ		.....C.....A.....C.....	1534
DNAPTFI		.....GC.....G.....G.....	1531
DNAPTR		.....T.....G.....A.....	1540
MAJORITY		GCTCCACGCCCCCTGCTGGAGCCCTXGGXGAGGCCACCCCATGGAGAACATGCTGCACTA	
DNAPTAQ		.....C.....G.....G.....	1604
DNAPTFI		.....T.....G.....A.....	1601
DNAPTR		.....G.....A.....G.....	1610
MAJORITY		GGGGAGCTACCAAGCTCAAGAACACCTACATXACCCCCCTGCCXGCTCGTCCACCCGAGGAGGGC	
DNAPTAQ		.....G.....G.....T.....T.....G.....A.....A.....	1674
DNAPTFI		.....A.....G.....C.....G.....A.....C.....	1671
DNAPTR		.....G.G.....G.....AAC.....G.....	1680
MAJORITY		CGCTCCACACCCCTTCAACGAGCGGCCACGGCAGGCTTAGCTCCACCCAACTGC	
DNAPTAQ		.....A.....T.....C.....	1744
DNAPTFI		.....G.....G.....TCC.....	1741
DNAPTR		.....G.....G.....	1750

FIG. 2F

MAJORITY	[SEQ ID NO:7]	AGAACATCCCCCTCCACCCXCTGGGAGGATCCCCCCCCCTCTGCCCCGGAGGXTGGGT
DNAPTAQ	[SEQ ID NO:1]	.....G.....G.....T.....G.....A.....G.....G.....C.....1814
DNAPTFI	[SEQ ID NO:2]	.....G.....T.....G.....C.....G.....A.....G.....1811
DNAPTR	[SEQ ID NO:3]	.....G.....T.....G.....T.....A.....G.....1820
MAJORITY		GTIGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTGGCCACCTCTGGGGACGAGAACCTG
DNAPTAQ	A.....	A.....G.....G.....C.....1884
DNAPTFI	C.....	T.....C.....T.....T.....1881
DNAPTR	.....A.....	G.....G.....A.....1890
MAJORITY		ATCGGGCTTCCAGGGGGAGGGACATCCACACCCAGACGCCAGCTGGATGTTGGGGCTCCCCCGG
DNAPTAQ	.....	.....C.....GG.....G.....1954
DNAPTFI	.....	.....T.....T.....C.....1951
DNAPTR	.....A.....	.....A.....A.....A.....1960
MAJORITY		AGGCCGCTGACCCCTGATGCCGGGGGCCAAGACCATCAACTCGGGTCTACCCGATGTCGG
DNAPTAQ	.....	.....G.....G.....2024
DNAPTFI	A.....G.....A.....	T.....G.....2021
DNAPTR	.....	G.....G.....C.....2030
MAJORITY		CCACCCCTCTCCAGGACCTGCCATCCCTACGGAGGGCTGCCCTCATGACCCCTACTTCAG
DNAPTAQ	.....	.....A.....T.....CCA.....T.....2094
DNAPTFI	.....	.....GG.....T.....2091
DNAPTR	.....T.....A.....	.....G.....T.....A.....2100

FIG. 2G

FIG. 2H

MAJORITY [SEQ ID NO:7] GCGCTGGAGCTGGAGCTGGGAGGACTGGCTCTGGGAGGAGCTAG

DNAPTAQ [SEQ ID NO:1] ..... A ..... GA  
DNAPTF1 [SEQ ID NO:2] ..... GCG ..... T ..... GT .....  
DNAPTF2 [SEQ ID NO:3] ..... T ..... GT .....

**FIG. 3A**

MAJORITY	[SEQ ID NO:8]	MXAMPLFEPKGRLVLDGHHLAYRTFFALKGLTSRGEPVQAVYFAKSLLKALKEG-DANXWVFDAK
TAO PRO	[SEQ ID NO:4]	RG.....H.....H.....I.....V.....V..... 69
TFL PRO	[SEQ ID NO:5]	.....V.....V..... 68
TTB PRO	[SEQ ID NO:6]	.....YK.....F..... 70
MAJORITY		APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLGLXRLEVPGYEADDVLATIAKKAEEKEGYEVRI
TAO PRO		.....GG.....A.....S..... 139
TFL PRO		.....V.....F.....R..... 138
TTB PRO		.....FT.....L.....K..... 140
MAJORITY		TADBDLYQLLSPRIAVLHPFGYLITPAWLWEKYGLRPEOWDYLRAKGPPSDNLPGVKGIGEKTAXKLX
TAO PRO		.....K.....H.....D.....A.....T.....E.....R.....E..... 209
TFL PRO		.....E.....I.....Y.....A.....I.....A.....R..... 208
TTB PRO		.....V.....V.....H.....E.....F.....V.....L.....K..... 210
MAJORITY		EWGSLENLKNLDRVKP-XXREKIXAHMEDLXLXXLSXVRDOLPLEDFAXRREPREGRLRAFLERLEF
TAO PRO		.....A.....L.....AI.....L.....D.....K.....WD.....AK.....K.....R..... 278
TFL PRO		.....FOH.....O.....SL.....LOG.....A.....RK.....Q.....H.....GR.....T.....NL..... 277
TTB PRO		.....ENV.....K.....L.....R.....LE.....R.....L.....L.....OG..... 280
MAJORITY		GSLLHEFGLEXPKALEEAPWPPPEGAFVGFLVLSRPEPMWAELLALAAARRXGRVHRAKDPLXGLRDLKEV
TAO PRO		.....S.....K.....D.....G.....PE.....YKA.....A..... 348
TFL PRO		.....G.....A.....L.....SF.....G.....WE.....L.....Q.....R.....G..... 347
TTB PRO		.....A.....AP.....K.....G.....D.....A.....A.....K..... 350

FIG. 3B

MAJORITY	[SEQ ID NO:8]	RGLI AKDLA VIAL BREG LDX PGDD PM LAY LDP SNT PEGUARRY GG EWTEA GERAL L SERL FXNLXX
TAQ PRO	[SEQ ID NO:4]	S. G. P. E. A. A. A. WG 418
TFL PRO	[SEQ ID NO:5]	I. F. E. A. A. OT. KE 417
TTR PRO	[SEQ ID NO:6]	S. V. A. H. H. R. LK 420
MAJORITY		RLEGEER LLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAAEEIRRLEEVFRLAGHPFNLNSRD
TAQ PRO		R. R. A. R. A. A. A. 488
TFL PRO		K. E. R. EA. V. O. 487
TTR PRO		K. H. L. 490
MAJORITY		QLERVLFDELGLPAIGKTEKTGKRSTSAANVLEALREAHPIVEKILROYRELTKLKNTYIDPLPXLVHPRTC
TAQ PRO		S. D. I. 558
TFL PRO		D. R. A. K. 557
TTR PRO		R. L. Q. H. V. S. 560
MAJORITY		RLHTRFNOTATATGRLSSSDPNLONIPVRTPLGORIRR AFAEGWXLWALDYSQIELRVLAHLSGDENL
TAQ PRO		I. I. 628
TFL PRO		V. V. 627
TTR PRO		A. A. 630
MAJORITY		IRVFQEGRDIHTOTASWMF GVPPEAVDPLMRRAAKTIINFGVLYGMSAHRLSQELAI PYEEAVAFIERYFO
TAQ PRO		E. R. O. 698
TFL PRO		S. G. G. S. 697
TTR PRO		K. V. 700

FIG. 3C

MAJORITY [SEQ ID NO:8] SFPKVRAWI EKILEGRRGGYVETLFGRRRYVPLNARVKSREAAERMAFNMPVQGTAADL MKLAMWKL

TAQ PRO	[SEQ ID NO:4]	E	768
TFL PRO	[SEQ ID NO:5]	Y	R.
TRH PRO	[SEQ ID NO:6]	G	767
		K	770

MAJORITY FPRLXEMGARMILQVHDELVLEAPKXRAEXVAALAKEVME GYVYPLAVPLEEVNGXGEDWLSAKEY

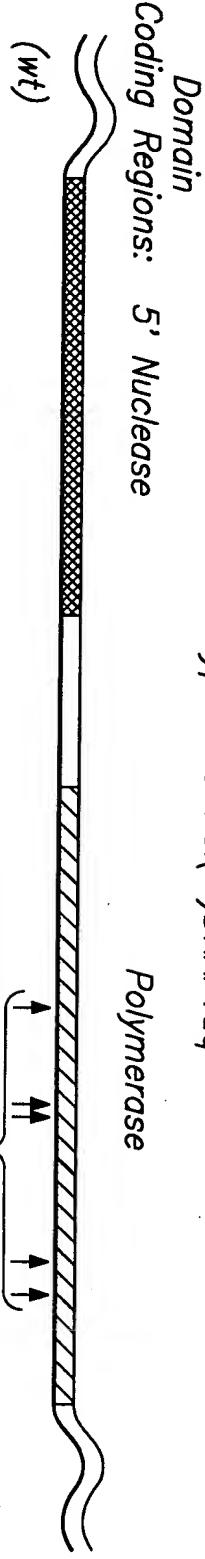
TAQ PRO	E	E	833
TFL PRO	Q	A.	831
TRH PRO	L	R.	835

Genes for Wild-Type and *PoI(-)DNAPTag*

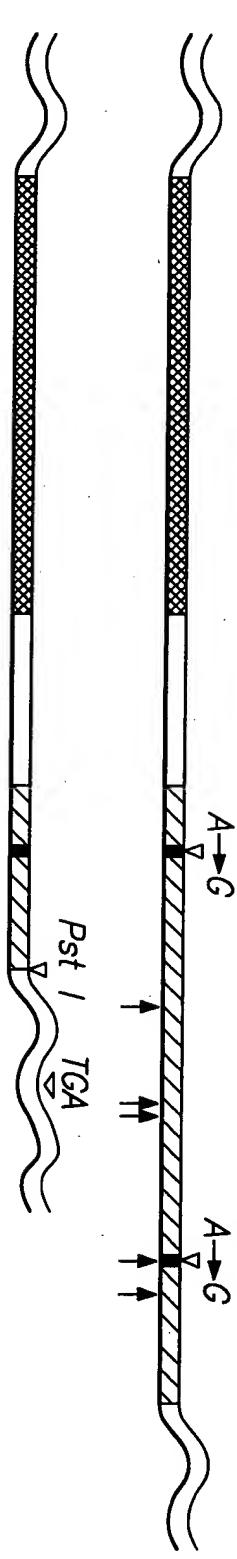
*Domain*  
Coding Regions: 5' Nuclease

Polymerase

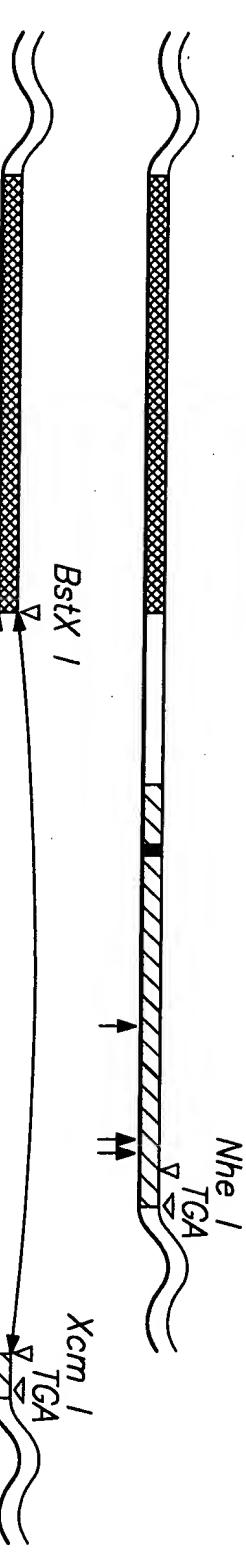
**FIG. 4A**



**FIG. 4B**  
**FIG. 4C**



**FIG. 4D**  
**FIG. 4E**

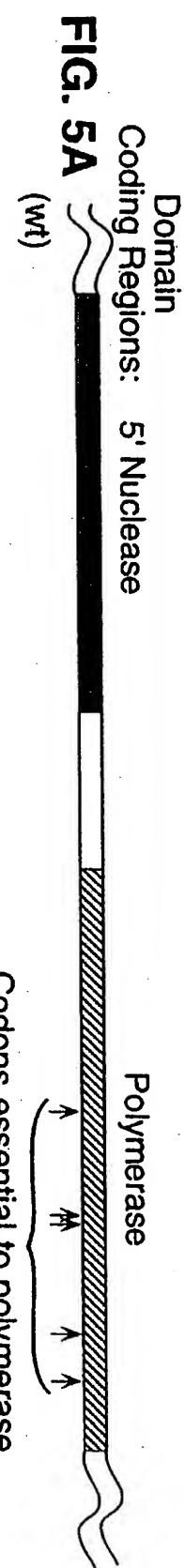


**FIG. 4F**



**FIG. 4G**

Genes for Wild-Type and Pol(-) DNAP<sub>T</sub><sup>fl</sup>



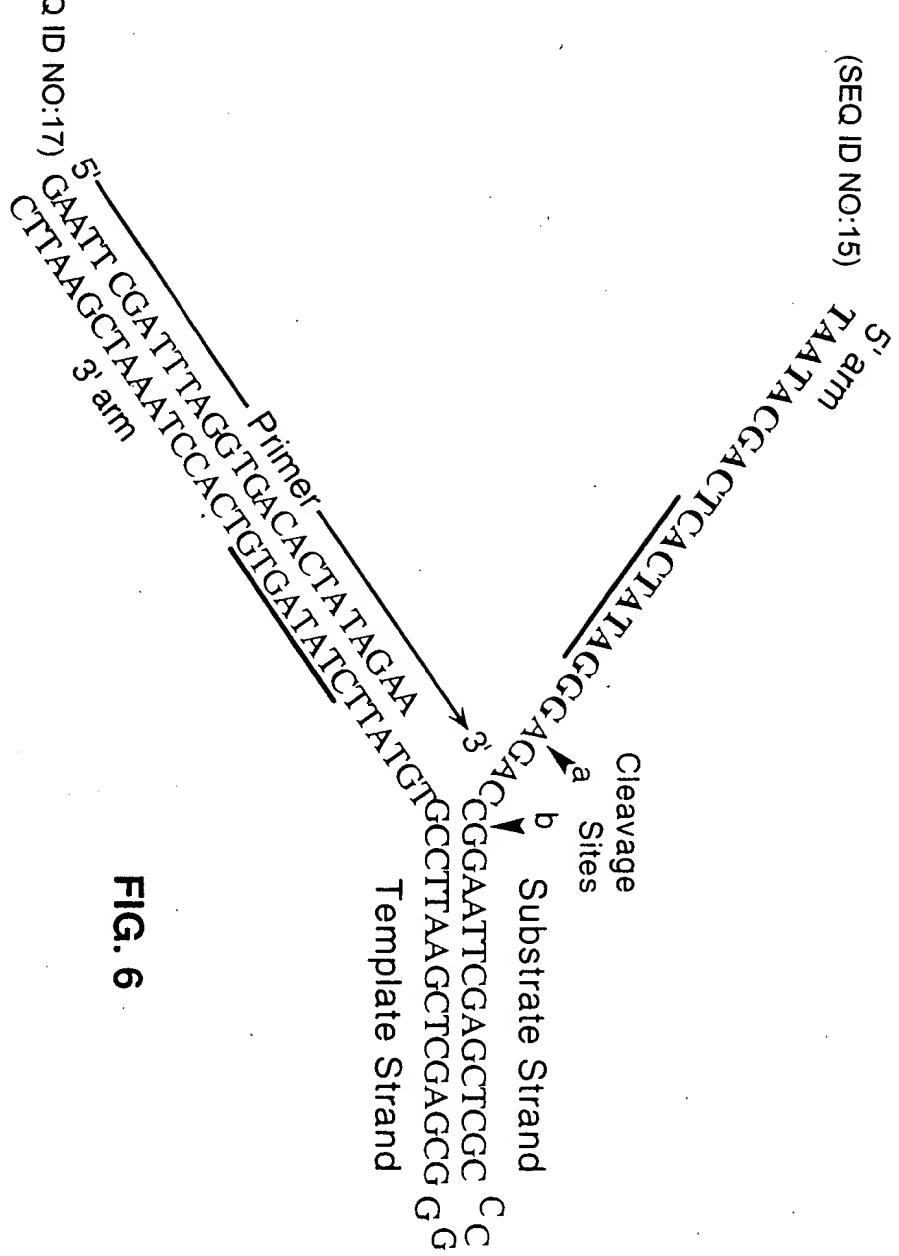
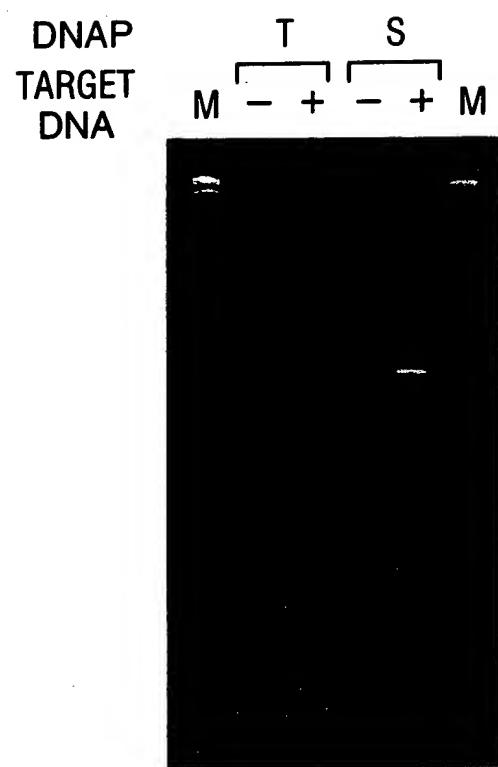
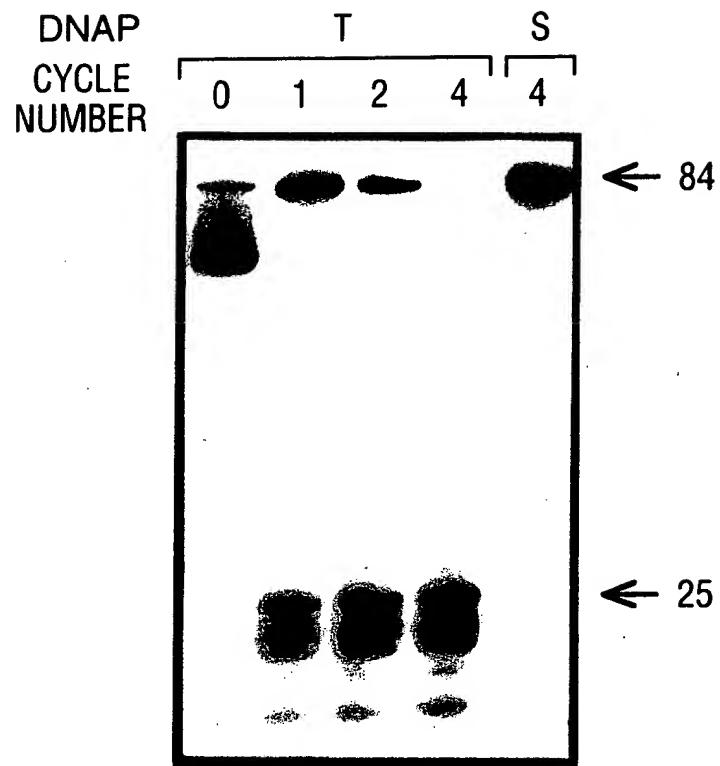


FIG. 6

"Replacement Sheet" ]

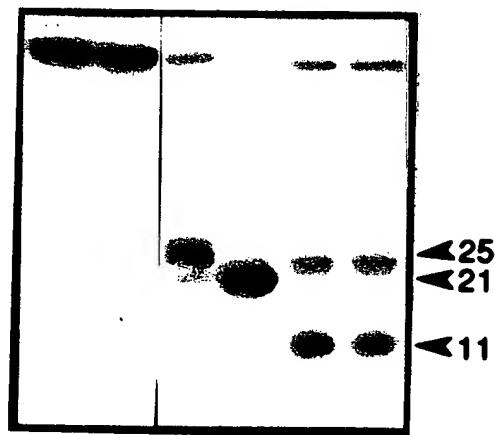


**FIG. 7**

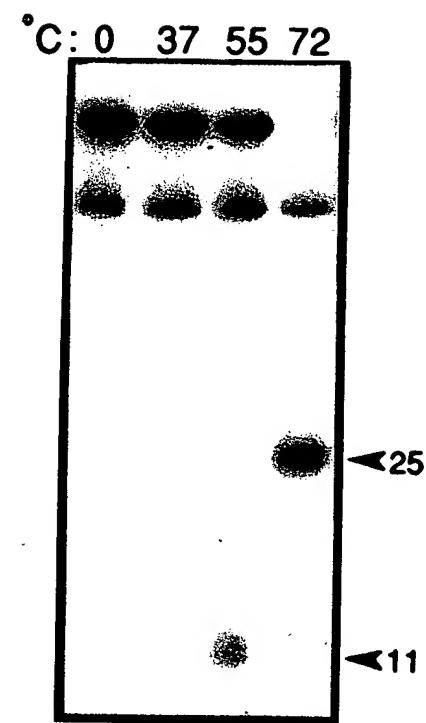


**FIG. 8**

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-



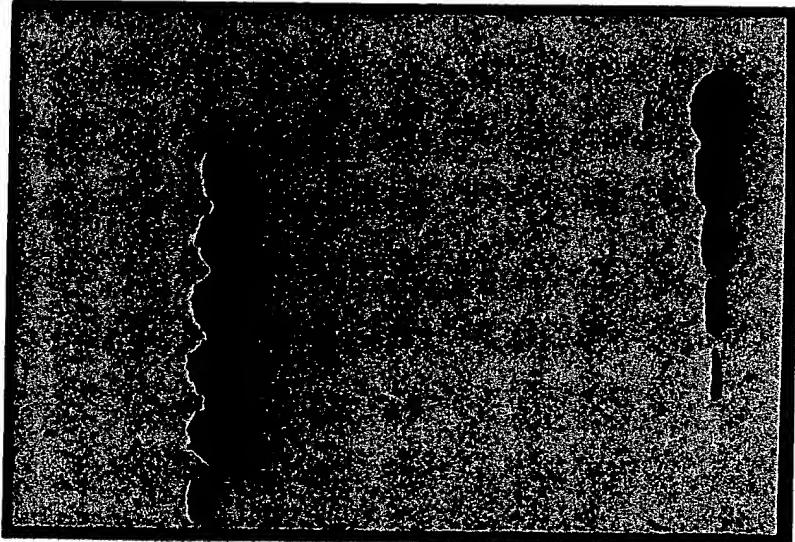
**FIG. 9A**



**FIG. 9B**

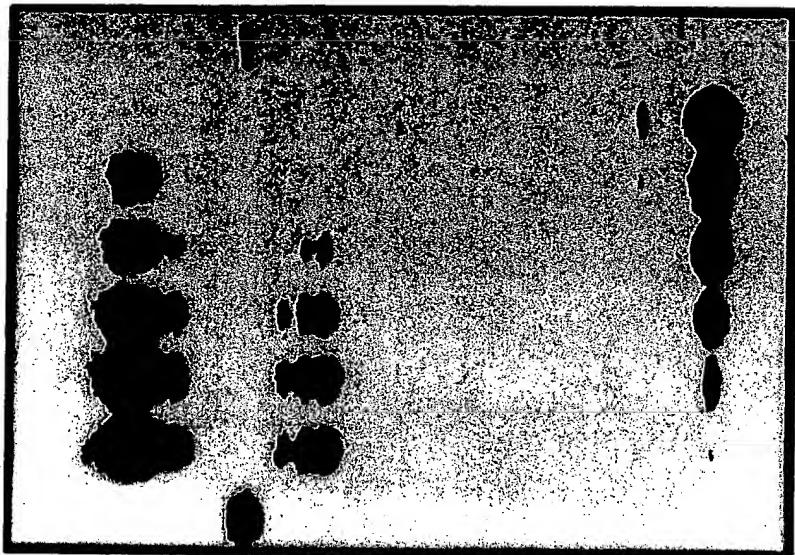
"Replacement Sheet"

$t$  (MIN): M 0 0.5 1 3 5 10 10 M



+ PRIMER

M 0 5 10 20 40 60 M



-PRIMER

FIG. 10A

FIG. 10B

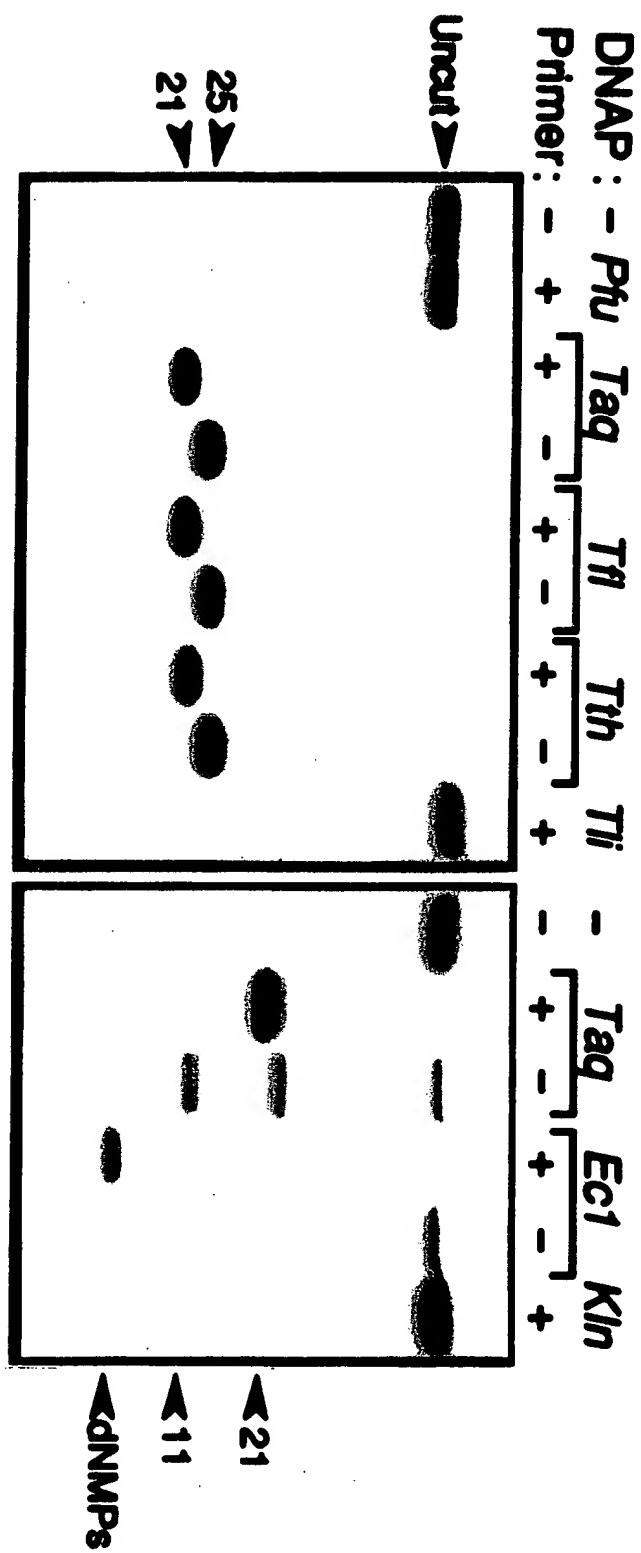
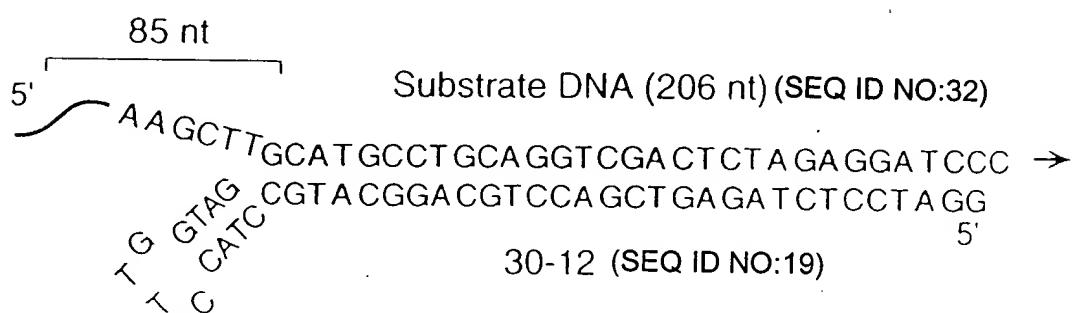
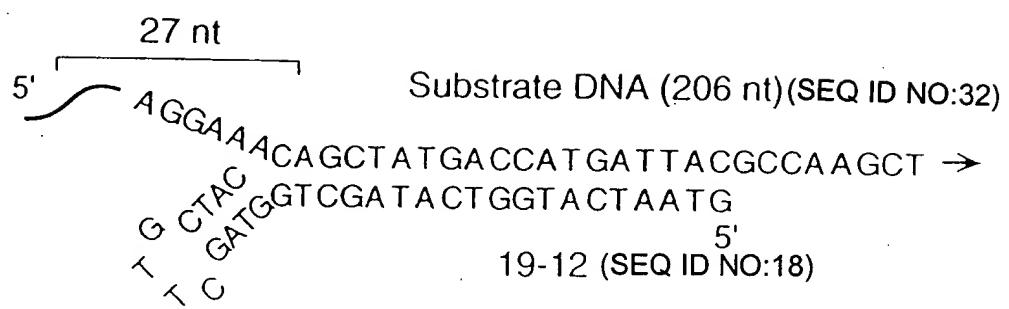
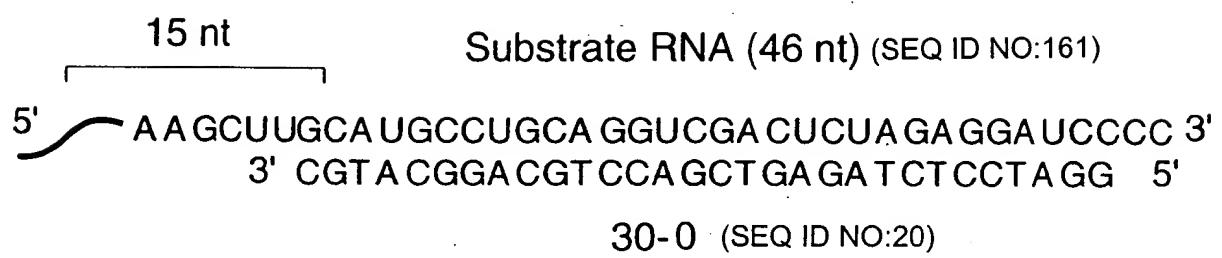


FIG. 12A





**FIG. 13A**

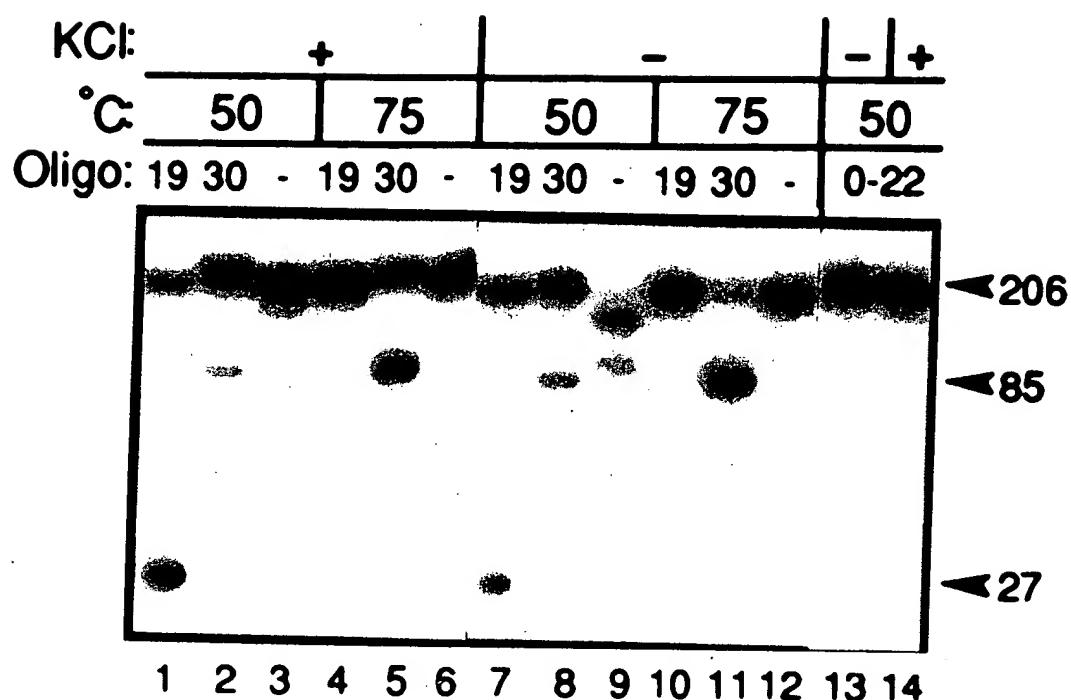


FIG. 12B

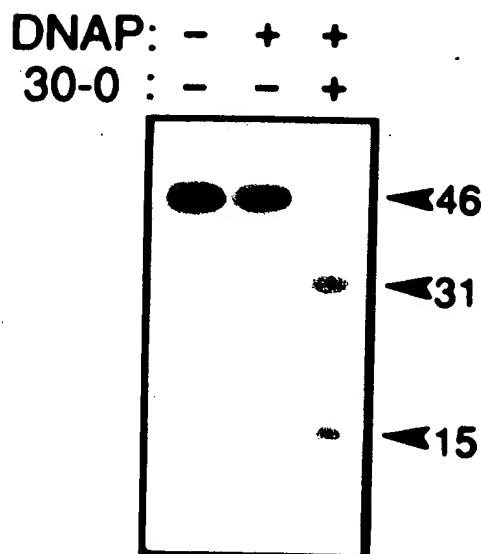


FIG. 13B

(SEQ ID NO:162)

-35  
TTGACATTAACATCGGCTCGTATAATGTGGAATGTGAGCGGATAACAATTCACACAGGAACAGCG  
 -10  
 RBS  
 MetAsnSer...  
 ATGAATTCGGAGCTCGGTACCCGGGATCCTCTAGAGTGACCTGCAGGCATGCAAGGCTTGGCACTGCC  
 EcoRI \_\_\_\_\_ KpnI \_\_\_\_\_ BamHI \_\_\_\_\_ Sall \_\_\_\_\_ PstI \_\_\_\_\_ SphI \_\_\_\_\_  
 SstI \_\_\_\_\_ SmaI \_\_\_\_\_ XbaI \_\_\_\_\_ HindIII

FIG. 14B

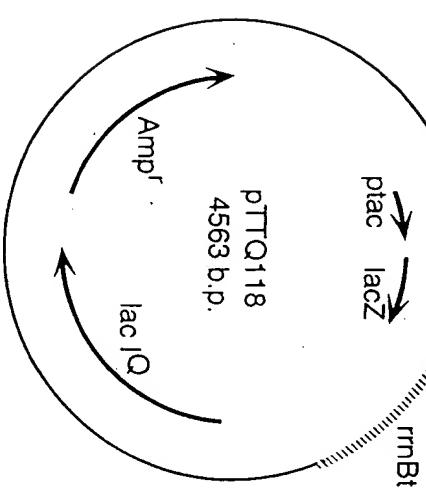


FIG. 14A

RBS: Ribosome binding site  
 ptac: Synthetic tac promoter  
 lac IQ: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment  
rrnBt: *E. coli* rrnB transcription terminator

FIG. 14C

(SEQ ID NO:163)

AGATCTCGATCCCGCGAAATTAA TACGACTCACTATAGGGAGACCACAA CGGTTCCCTCTAGAAATAATTGTTT  
Bgl II T7 Promoter XbaI

MetAlaSer  
AACTTAAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGGATCCGGCT  
RBS NdeI

T $\phi$   
BamHI ←  
Bgl II ←  
BamHI

FIG. 15B

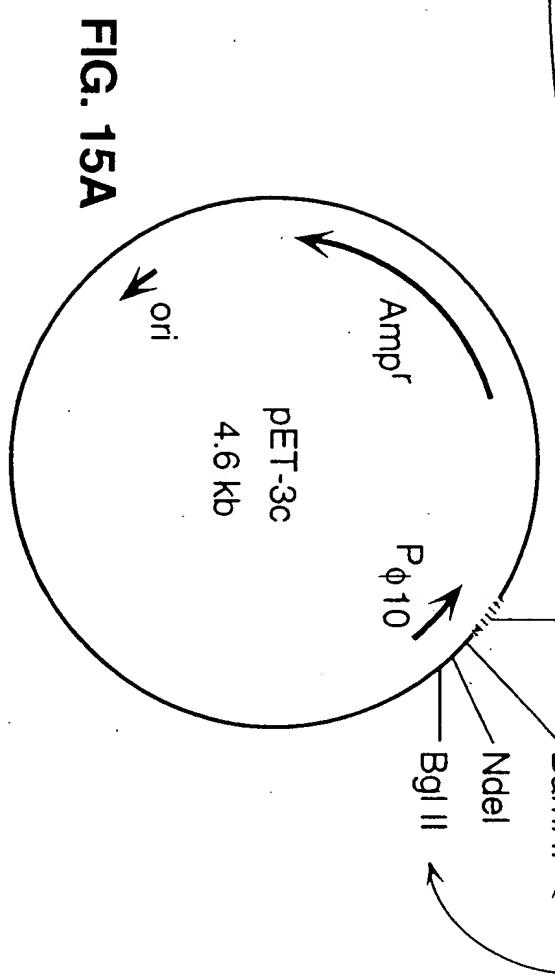
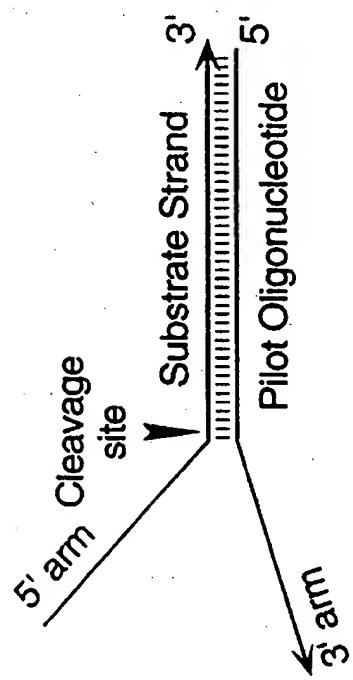


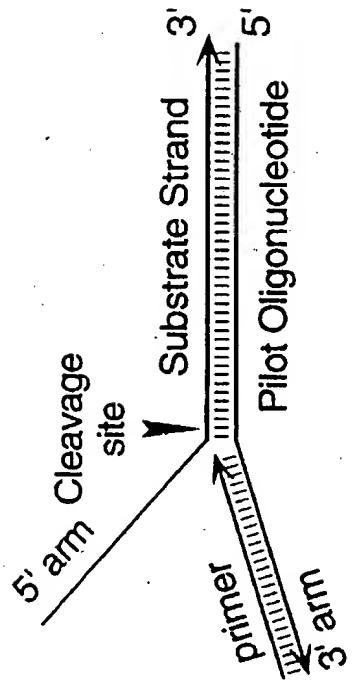
FIG. 15A

$P_{\phi 10}$ : Bacteriophage T7  $\phi 10$  promoter  
 $T\phi$ : T7  $\phi$  Terminator  
RBS: Ribosome binding site

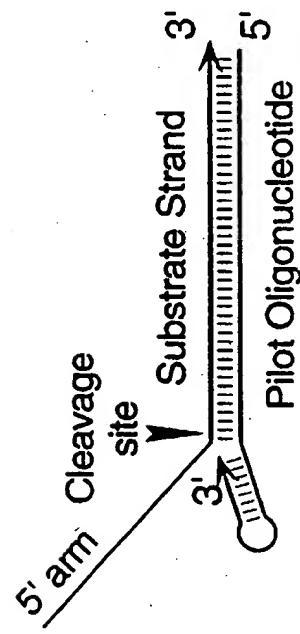
FIG. 15C



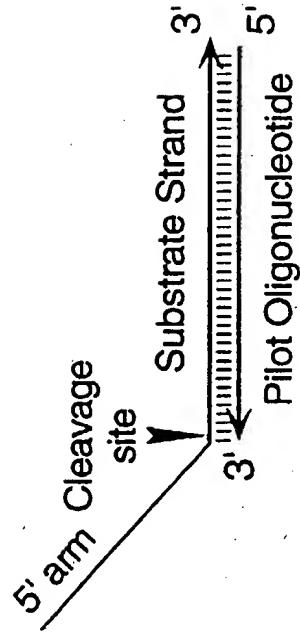
**FIG. 16A**



**FIG. 16B**



**FIG. 16C**



**FIG. 16D**

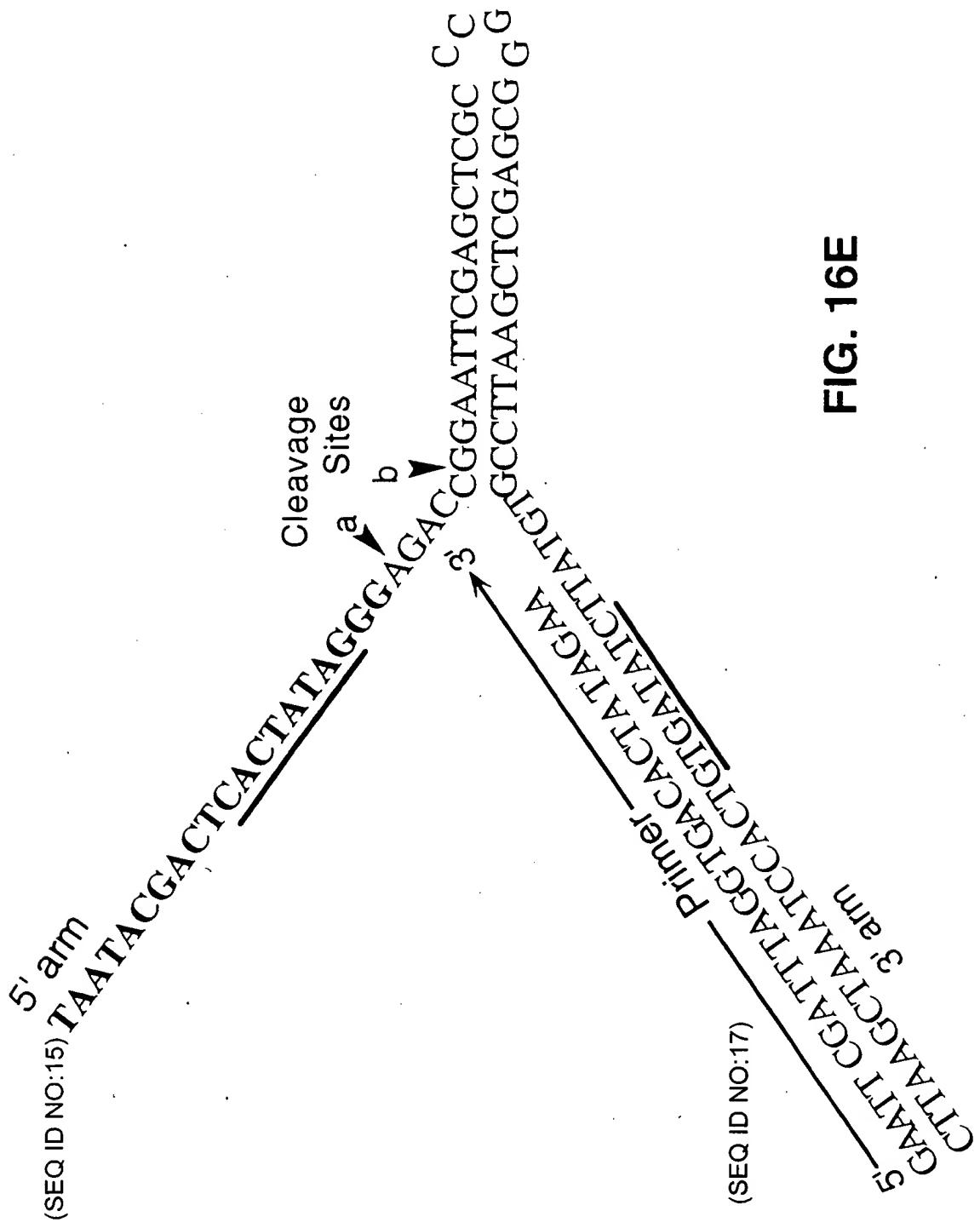


FIG. 16E

1 2 3 4 5 6 7

} UNCLEAVED SUBSTRATE

} CLEAVED SUBSTRATE

- - - + - - + dNTPs  
- - + + - - + PRIMER  
Taq 4e 5b ENZYME

"Replacement Sheet"

**FIG. 17**

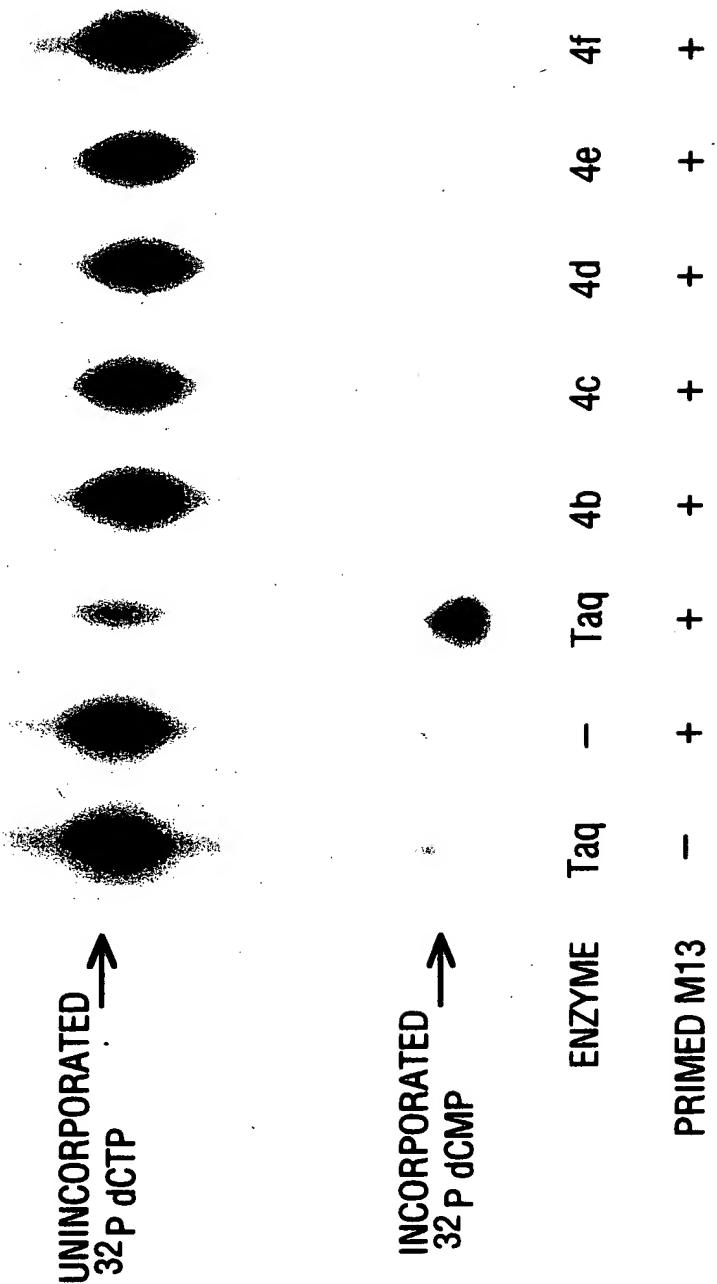


FIG. 18

## "Replacement Sheet"

(<sup>32</sup>P) 

5' (SEQ ID NO:164)

Sites of Cleavage with a gap of 6 nt.

60%  40% 

5' (SEQ ID NO:22)

GATTAGGTGACACTATAG

3' CTTAAGCTAAATCCACTGTGATATCTTATGTGCCTTA

3' T C A G

**FIG. 19A**

		"4d"		"4b"		UNMODIFIED	
		NO POL. ACTIVITY		MUTATION SMALL ACTIVITY		DNAP Taq	
1	2	3	4	5	6	7	8
-	-	-	+	-	+	-	+

dNTP

84 NUC. —



← HAIRPIN TEST MODULE

← CONVERSION TO DOUBLE STRANDED  
(COMPLETE EXTENSION OF PRIMER)

DESIRED  
PRODUCT →  
21 NUC.

MULTIPLE BANDS  
} CAUSED BY POLYMERIZATION

FIG. 19B

↑ SOME ABERRANT CLEAVAGE WITH "4b"  
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

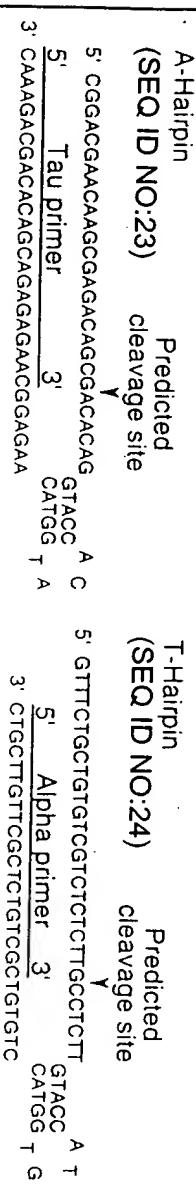


FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)  
5' GACGAAACAAGCGAGACAGGG 3'

FIG. 20B

3' CAAAGACGACAGCAGAGAACGGAGAA  
**FIG 20C** Cleaved A-Hairpin

FIG. 20C

(SEQ ID NO:28)

5' ACACAG G T A C  
 3' T A G G G A G A A  
 saved A-Hairpin  
 EQ ID NO:28)

2

MnII RsaI | RsaI/MspI KpnI

BsmAI (SEQ ID NO:31)

- 2 -

**FIG. 20D** A-Hairpin 5' GTTCTGCTGTGCTCTCTGCCTCTGTACCATGGTGTACCTGTCGCTGCTGTTGCT 3' CAAAGACACAGCAGAGAGAACATGGTACACCATGGACACAGCGACAGAGCGAACAGCAGGC 5'

(SEQ ID NO:23)

(SEQ ID NO:165)

CCCCAGGGTTTCCCCAGTCACGACGTTGTAACACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGAGCTCGGTACCCGGGATTCCTC  
 CGGGTCCCCAAAGGGTCAGTGCTGCCAACATTTGGTGGCCGCTCACTAACATTGCTGACTATCCCCCTTAAGGCTGAGCCATGGGCCCCTAGGAG

— 47 Forward —

— 77 —

— 30 —

— 30 —

— 48 Reverse —

— 48 Reverse —

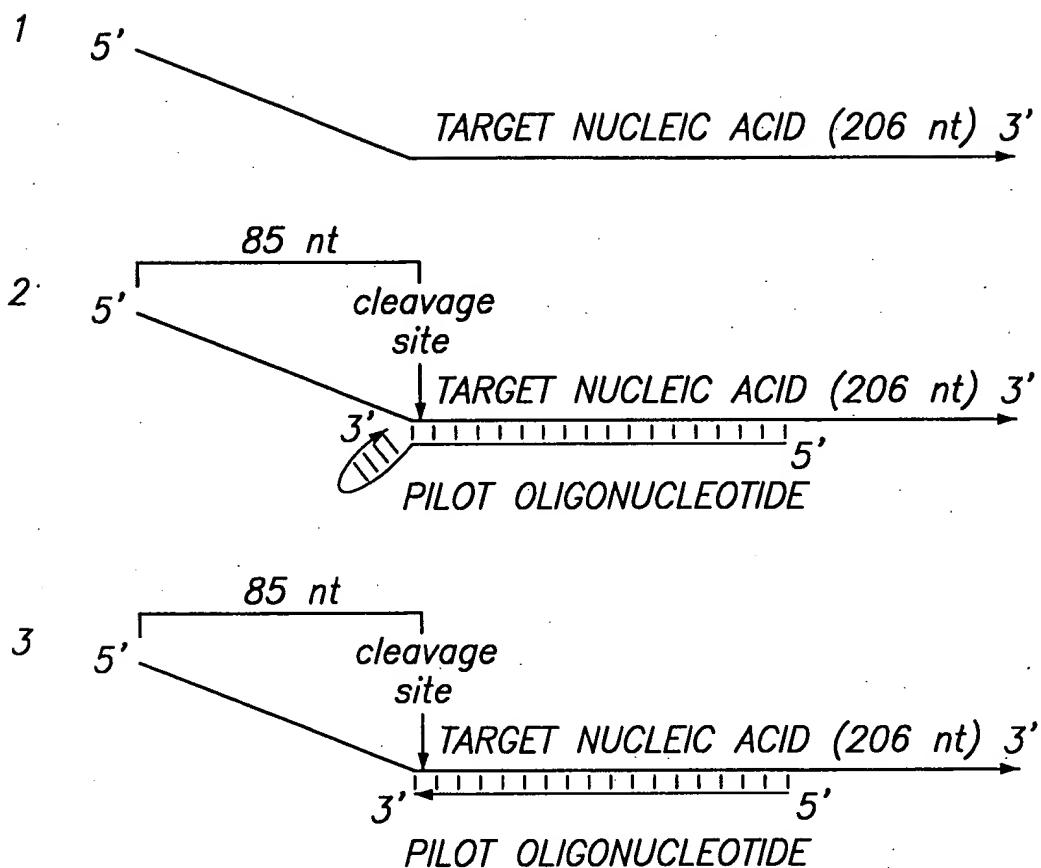
— 27 —

— 228 —

— 48 Reverse —

— 206 —

FIG. 21



**FIG. 22A**

## "Replacement Sheet"

	I	II	III	IV	V	I	VI
1	1	2	3	1	2	3	1
1	1	2	3	1	2	3	1
1	1	2	3	1	2	3	1
1	1	2	3	1	2	3	1

FIG. 22B

## "Replacement Sheet"

(SEQ ID NO:35)

5'

GACGAACAAAG CGAGACAGCCG

3'

(SEQ ID NO:34)  3'  
 (SEQ ID NO:33)  5' (SEQ ID NO:33)

(SEQ ID NO:36)

3' C TGGTCTCG TCTCTGGGT CTT FL 5'

(SEQ ID NO:37) 5' *FL* 3'  
  
 (SEQ ID NO:38)

5' FL GACCGAACAG CGAGACAGGG 3'  
(SEQ ID NO:35)

FIG. 23

CDR BEAD	T	T	T	A/T	A/T	A	A	A
PILOT	-	-	+	-	+	-	-	-
CLEAVASE	M	M	-	+	+	+	+	-

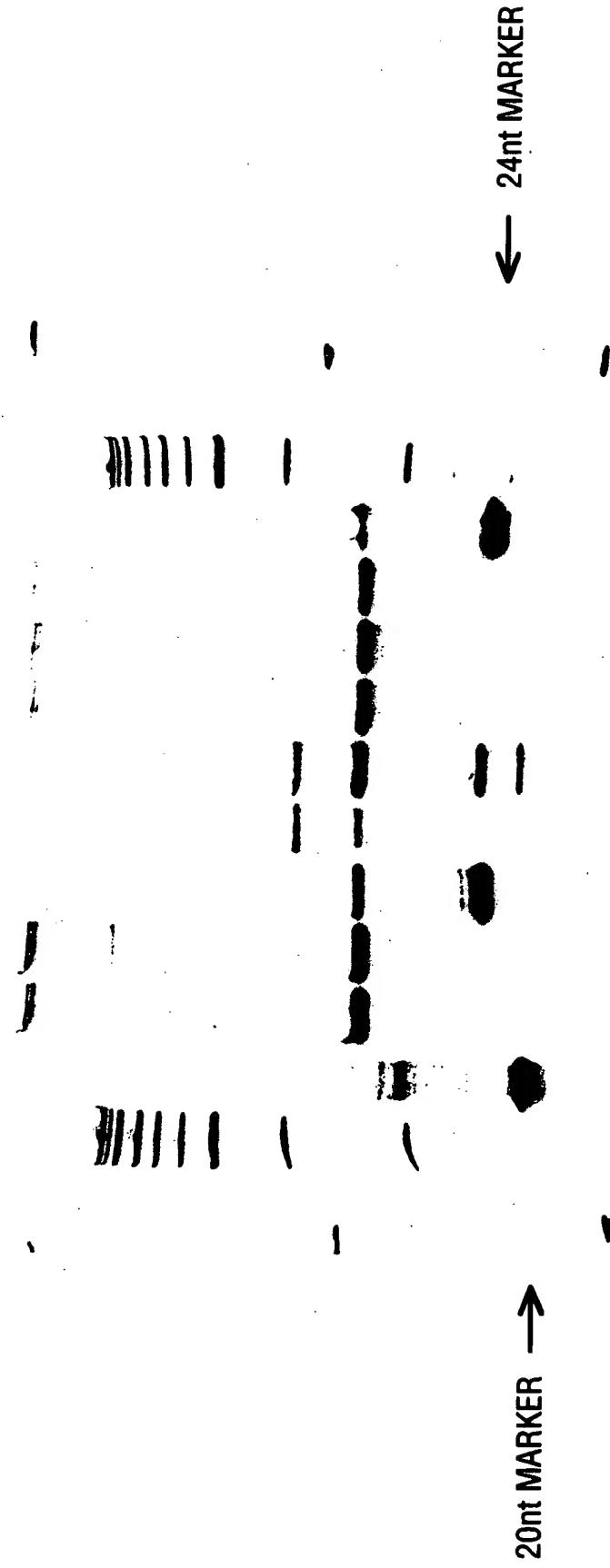
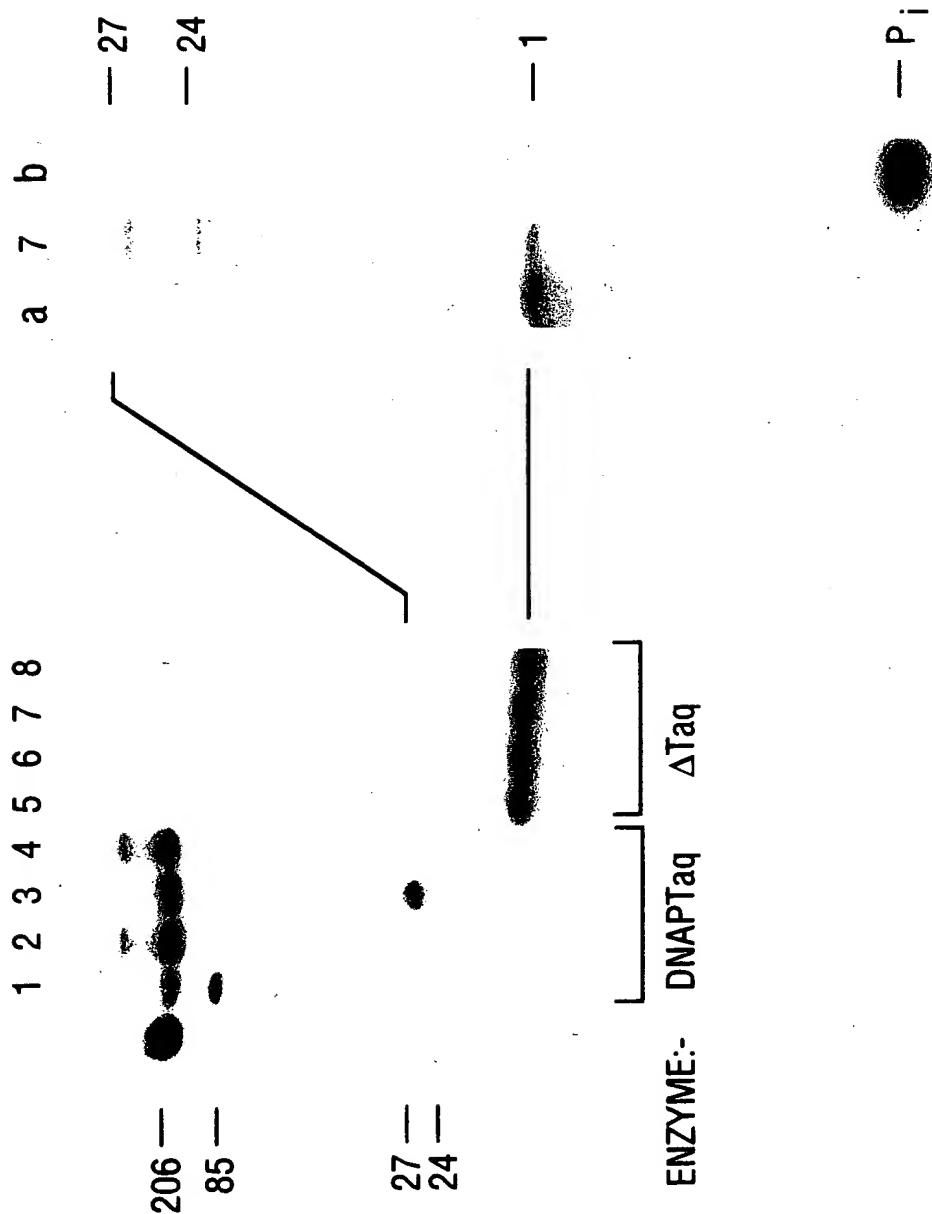


FIG. 24

## "Replacement Sheet"



## FIG. 25A

## FIG. 25B

FIG. 26A

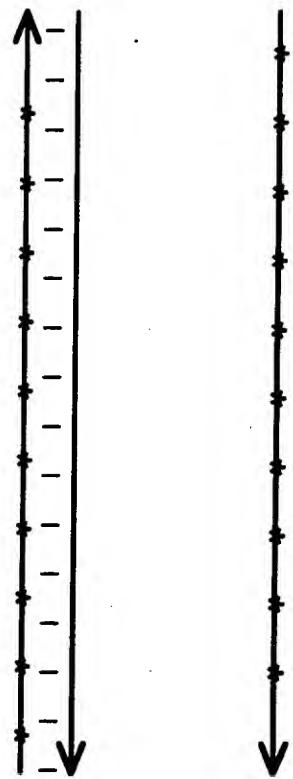
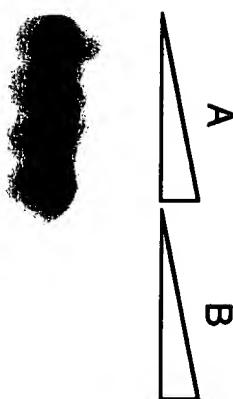
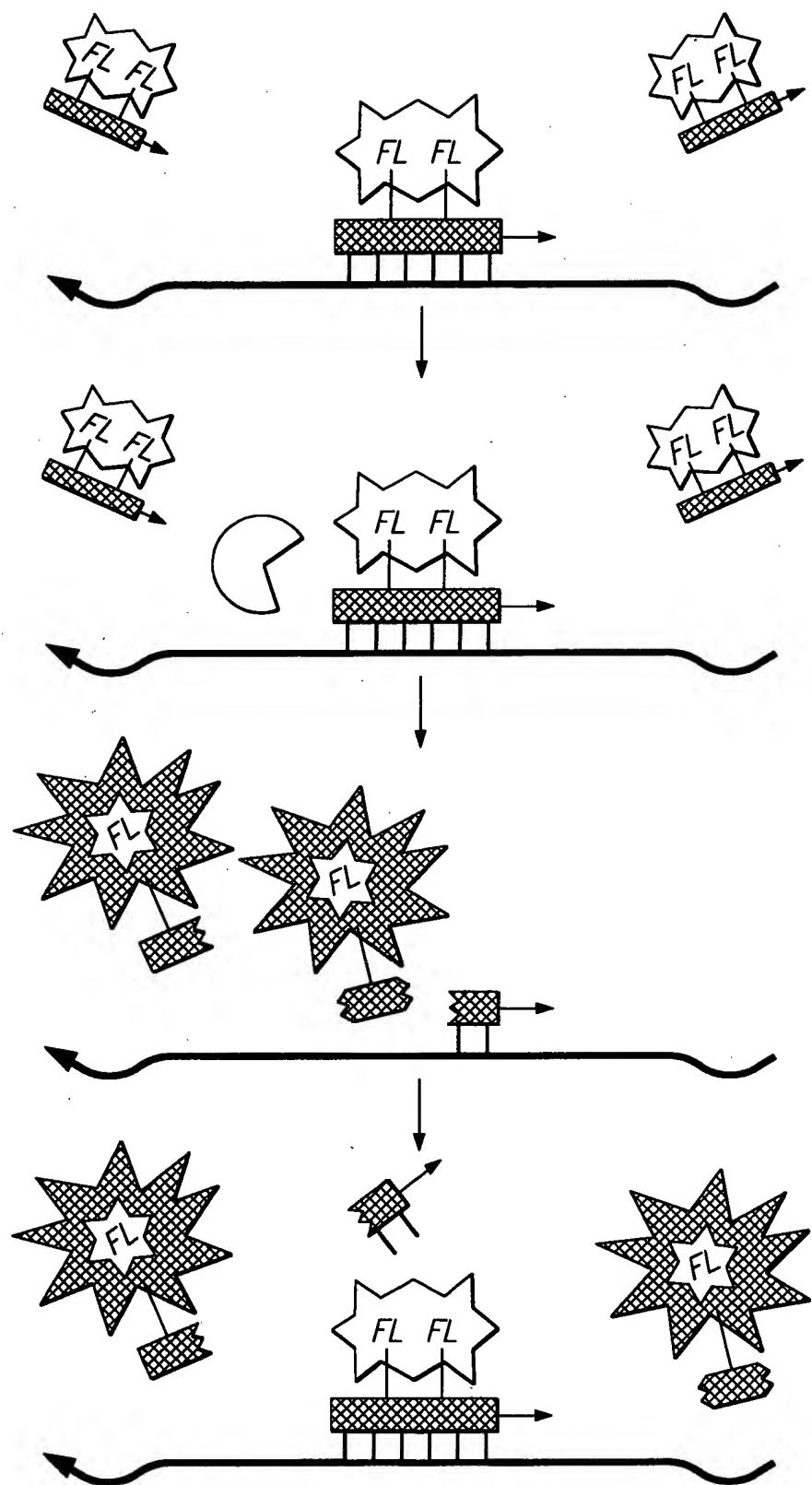


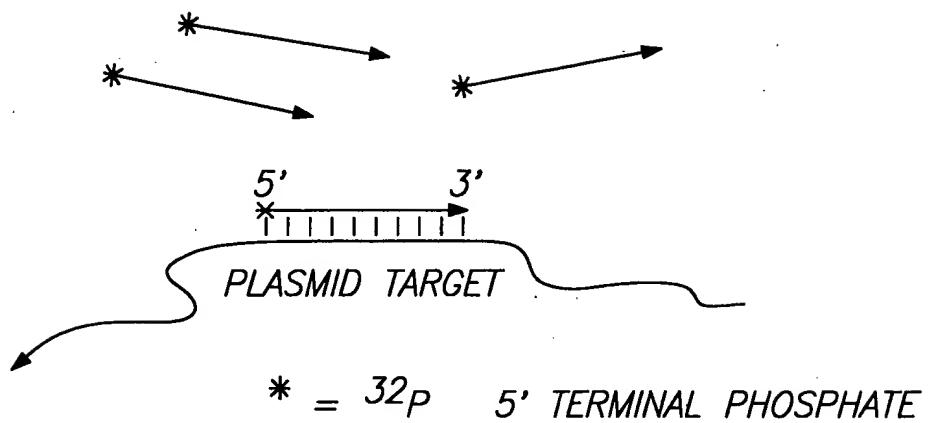
FIG. 26B

\* = 32p

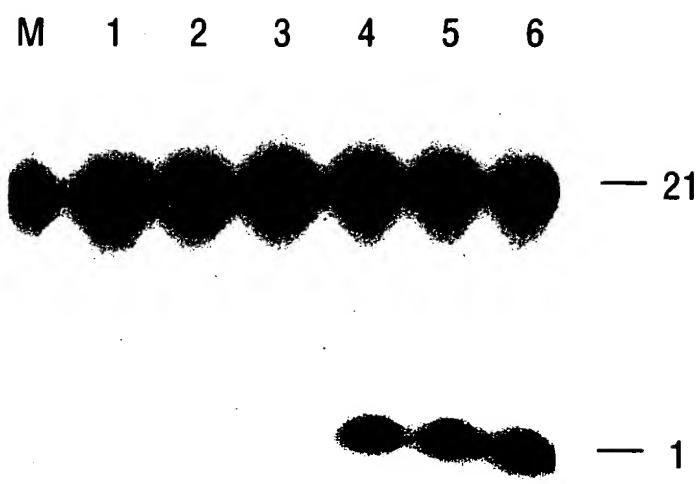




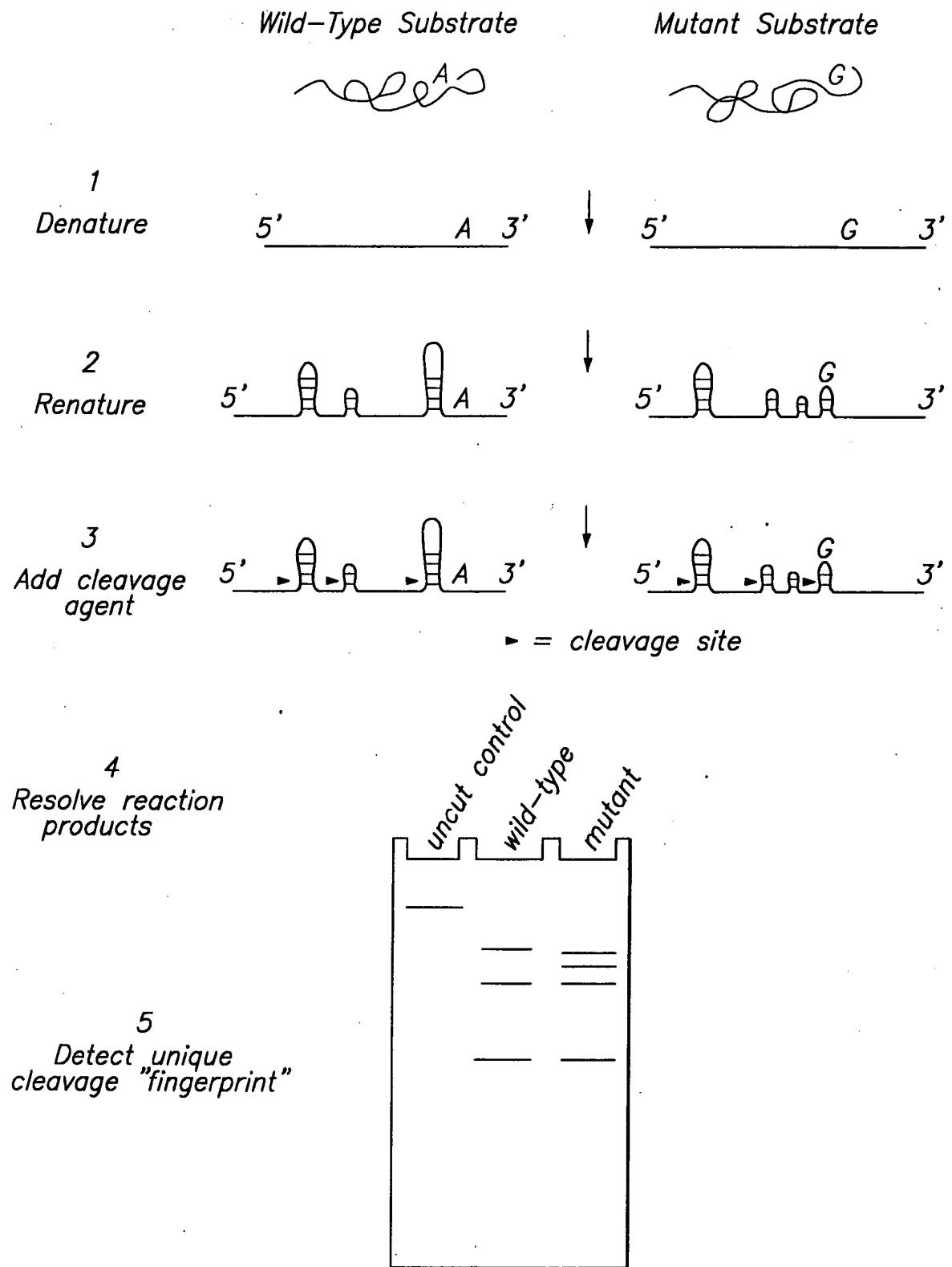
**FIG. 27**



**FIG. 28A**

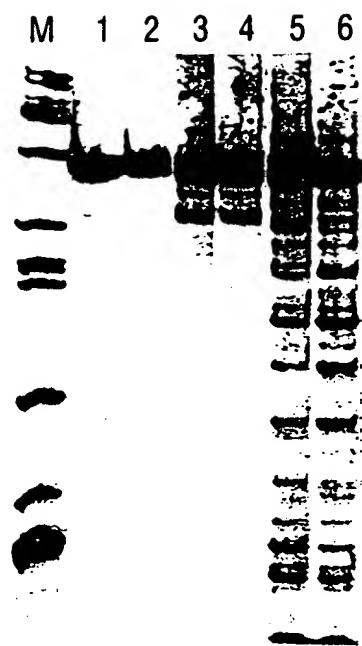


**FIG. 28B**

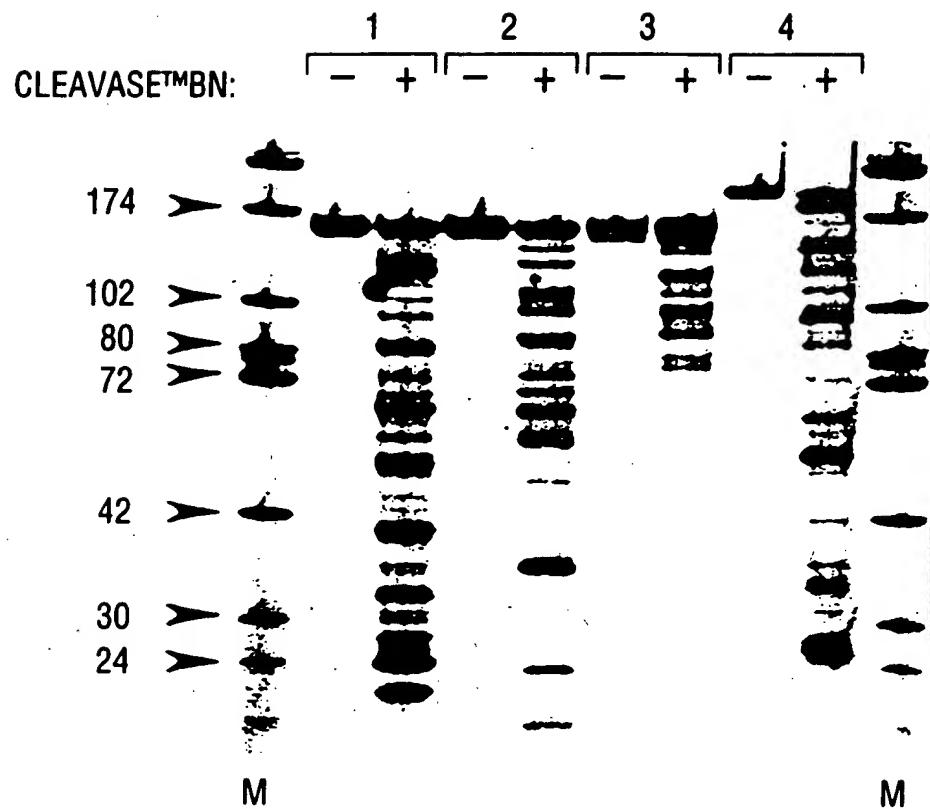


**FIG. 29**

"Replacement Sheet"



**FIG. 30**



**FIG. 31**

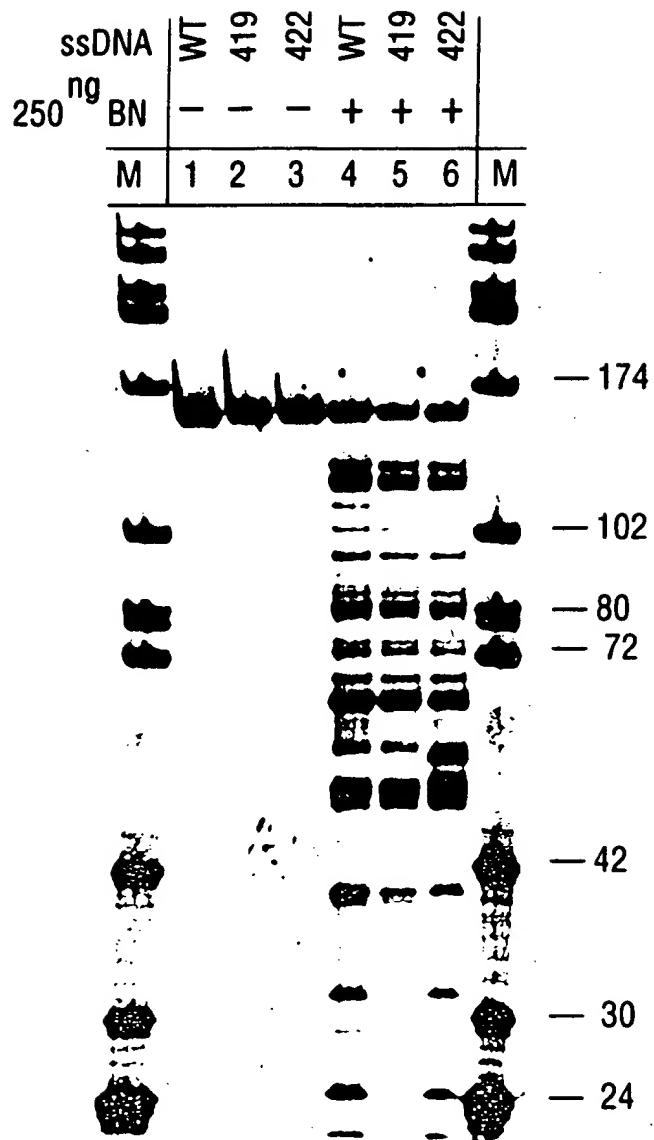


FIG. 32

"Replacement Sheet"

157 378 1056 1587  
M 1 2 3 4 5 6 7 8 M



WT 422  
WT 422  
WT 422  
WT 422

FIG. 33

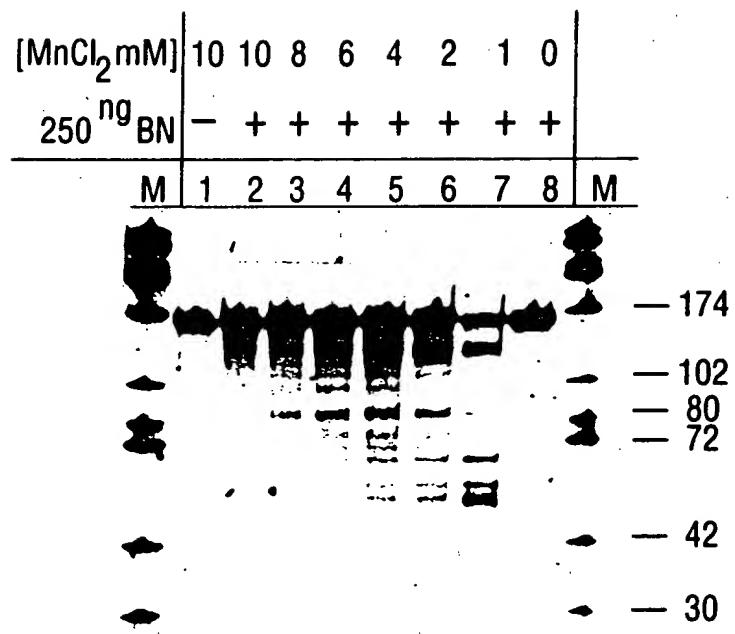
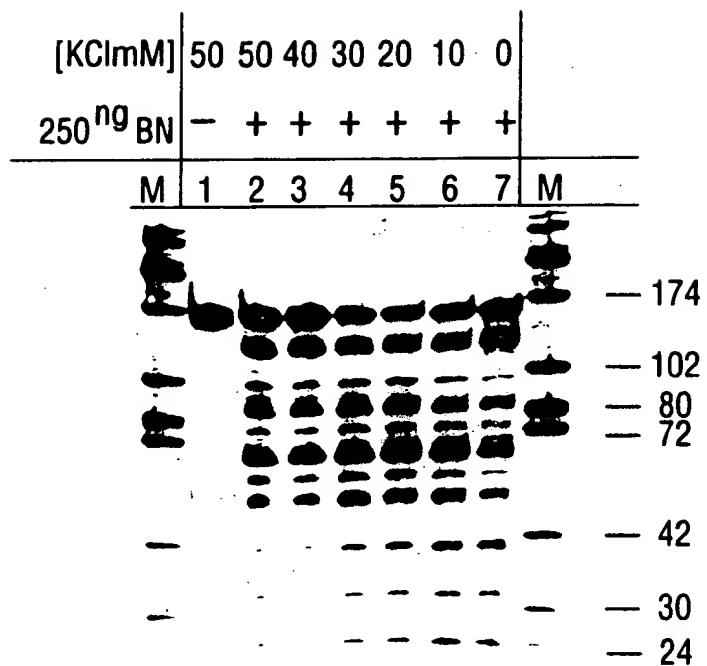


FIG. 34



**FIG. 35**

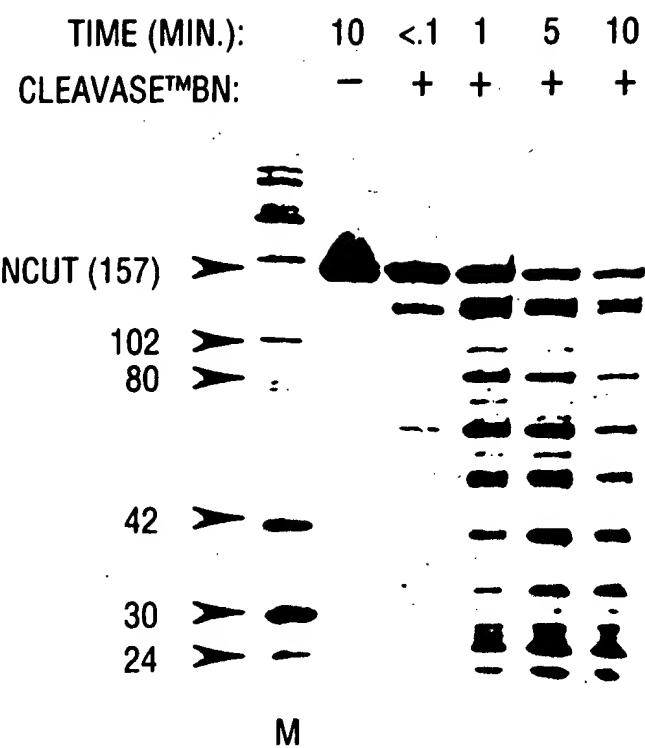


FIG. 36

TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	-	-	+	+	+	+	-	+

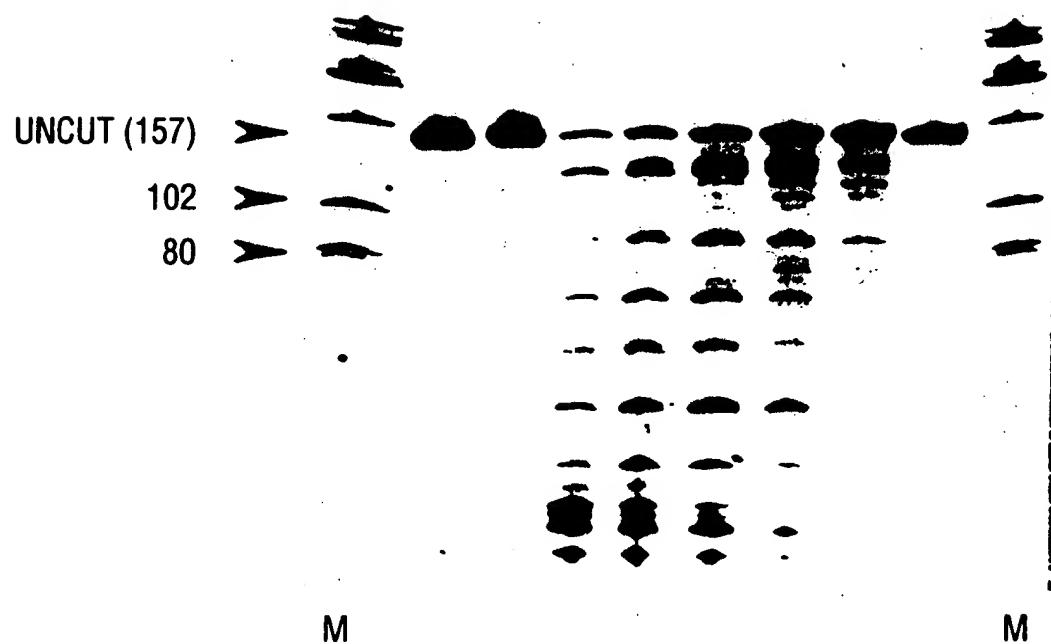


FIG. 37

CLEAVASE<sup>TM</sup>BN (ng): - 10 50 100 250



FIG. 38

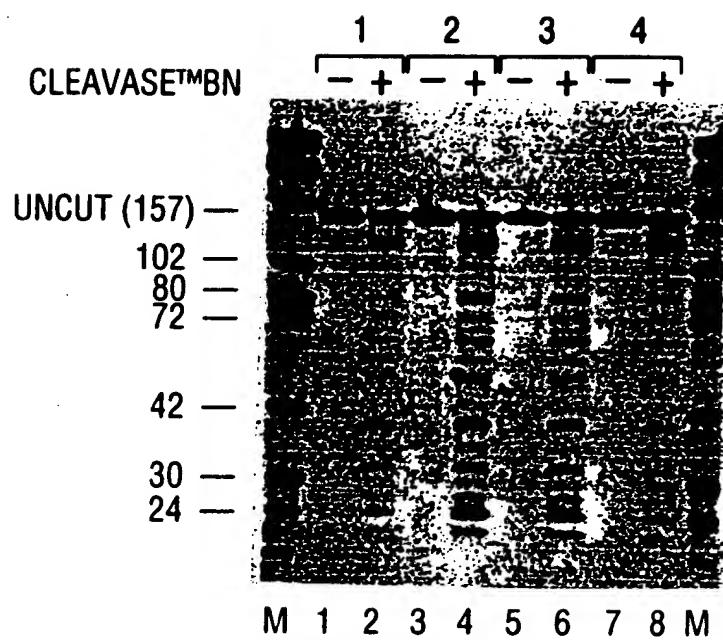


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND				5' - FLUORESCIN ANTI-SENSE STRAND				
	WT	419	422	WT	419	422	WT	419	422
ssDNA									
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	-
M	1	2	3	4	5	6	7	8	9
									10
									11
									12

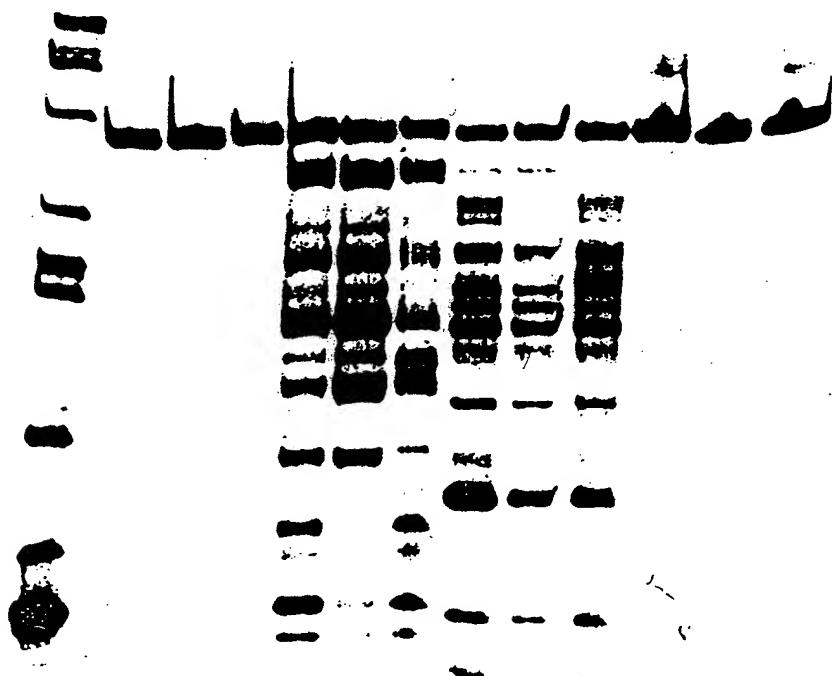


FIG. 40

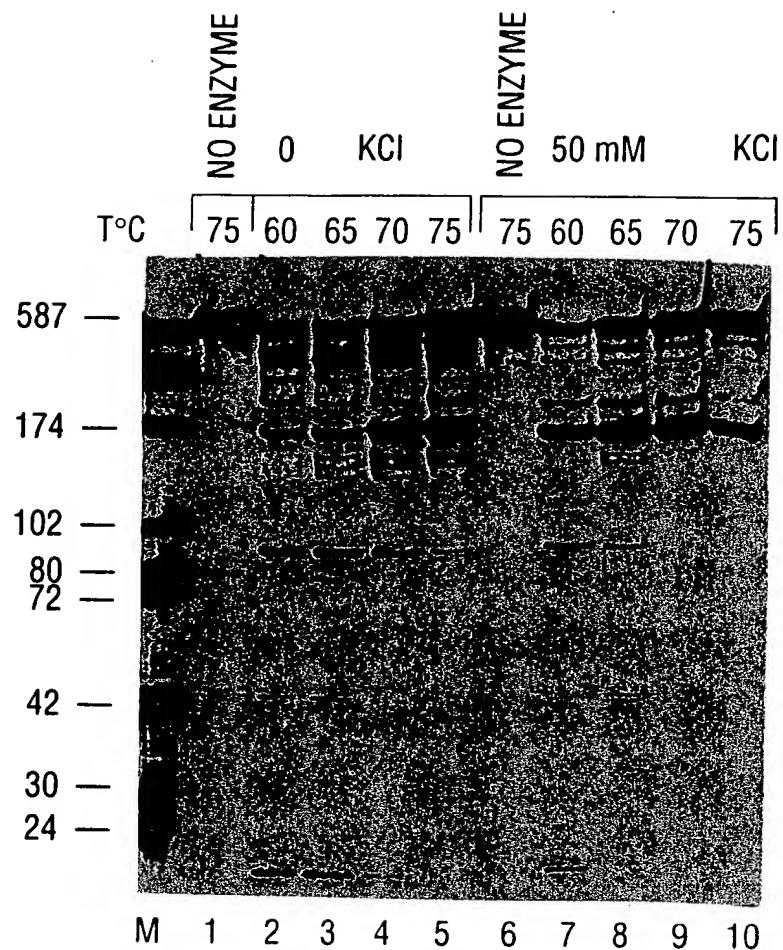


FIG. 41

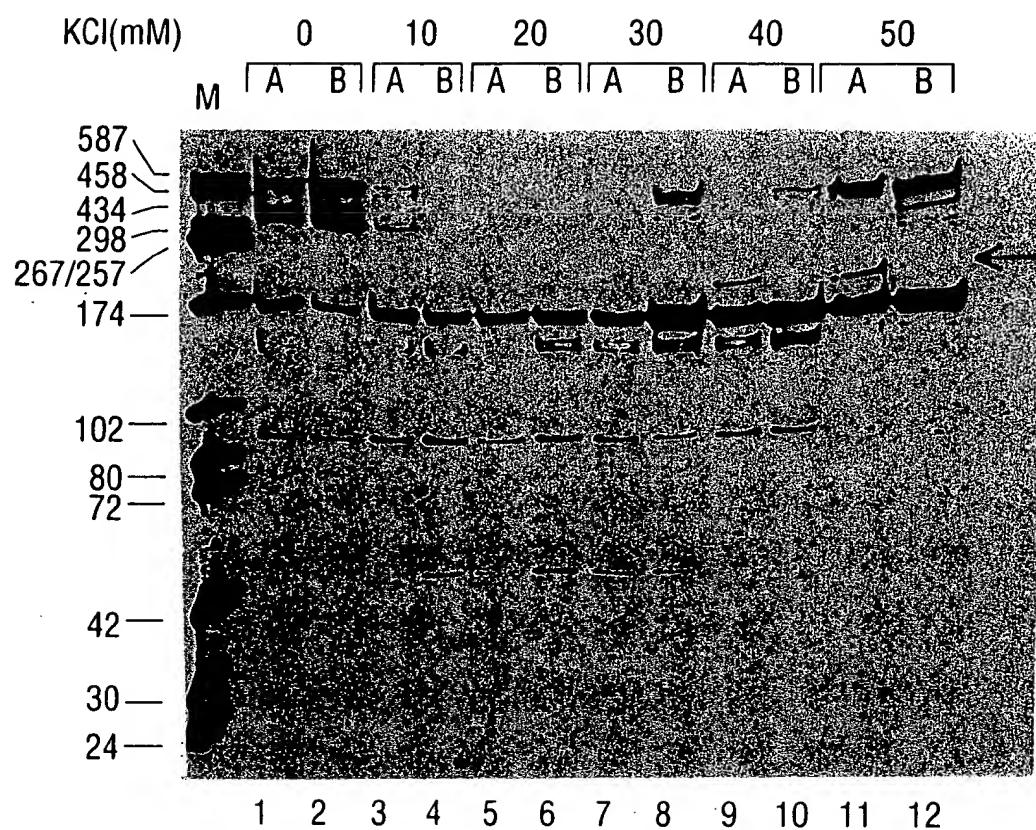


FIG. 42

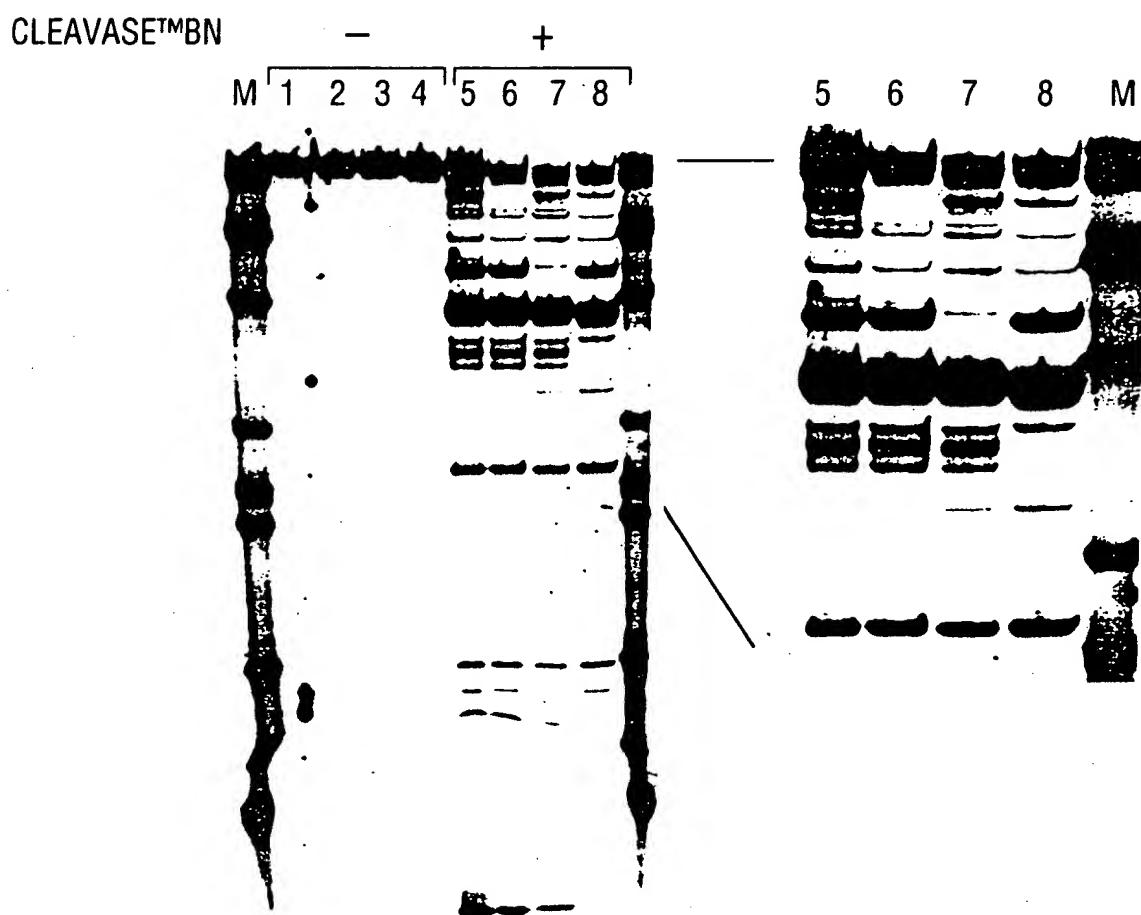


FIG. 43

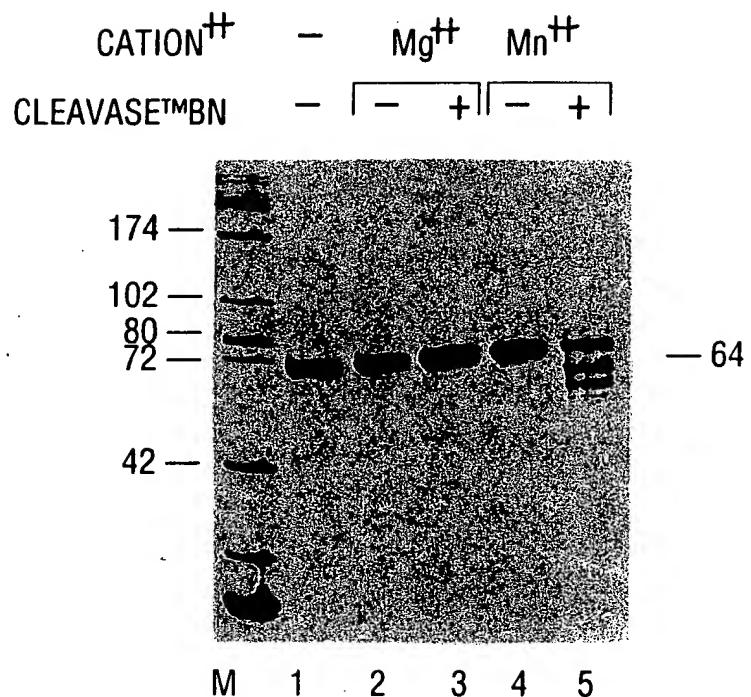


FIG. 44

"Replacement Sheet"

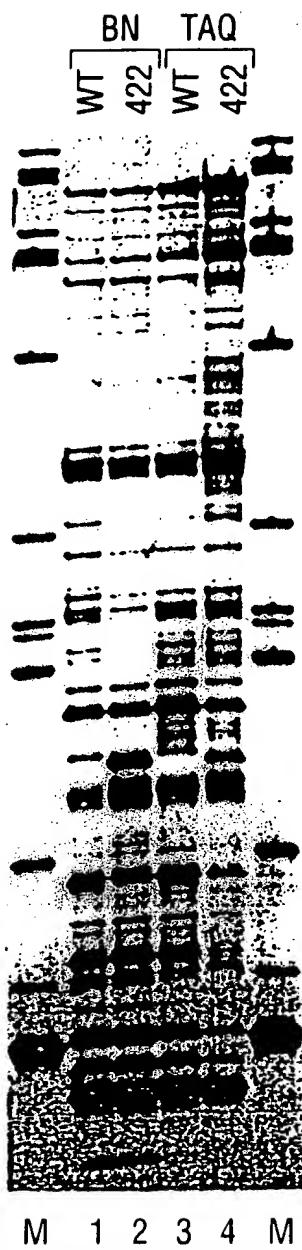


FIG. 45

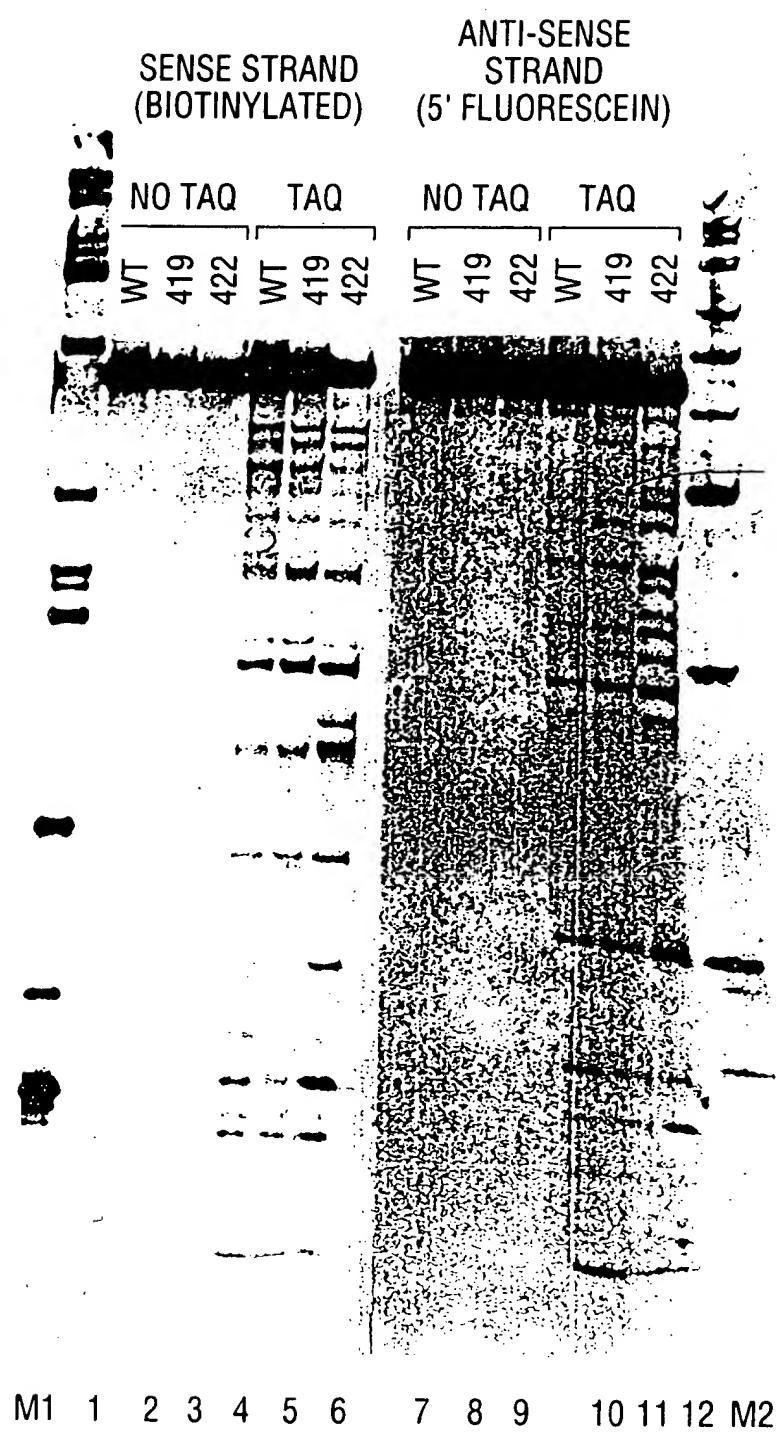
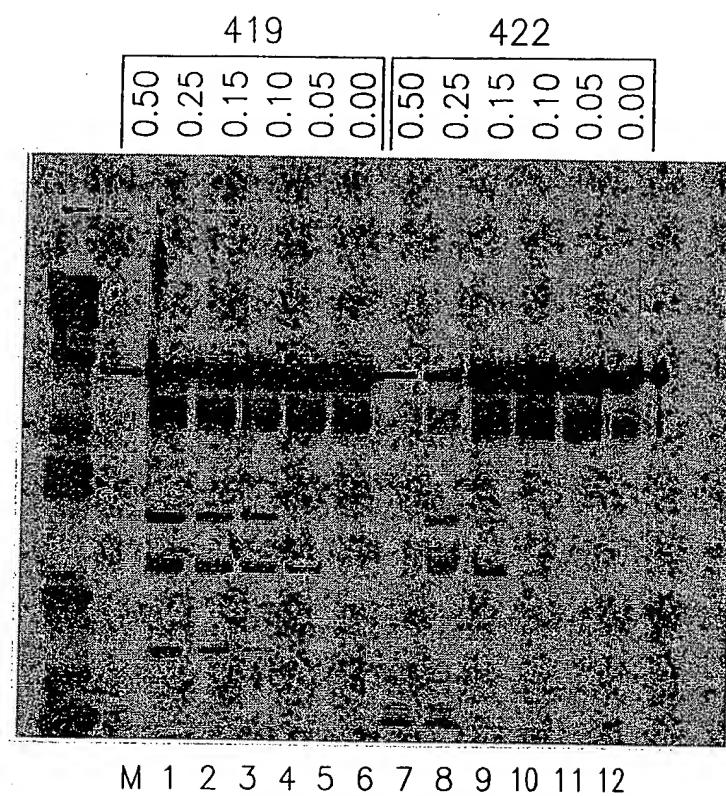


FIG. 46



**FIG. 47**

"Replacement Sheet"

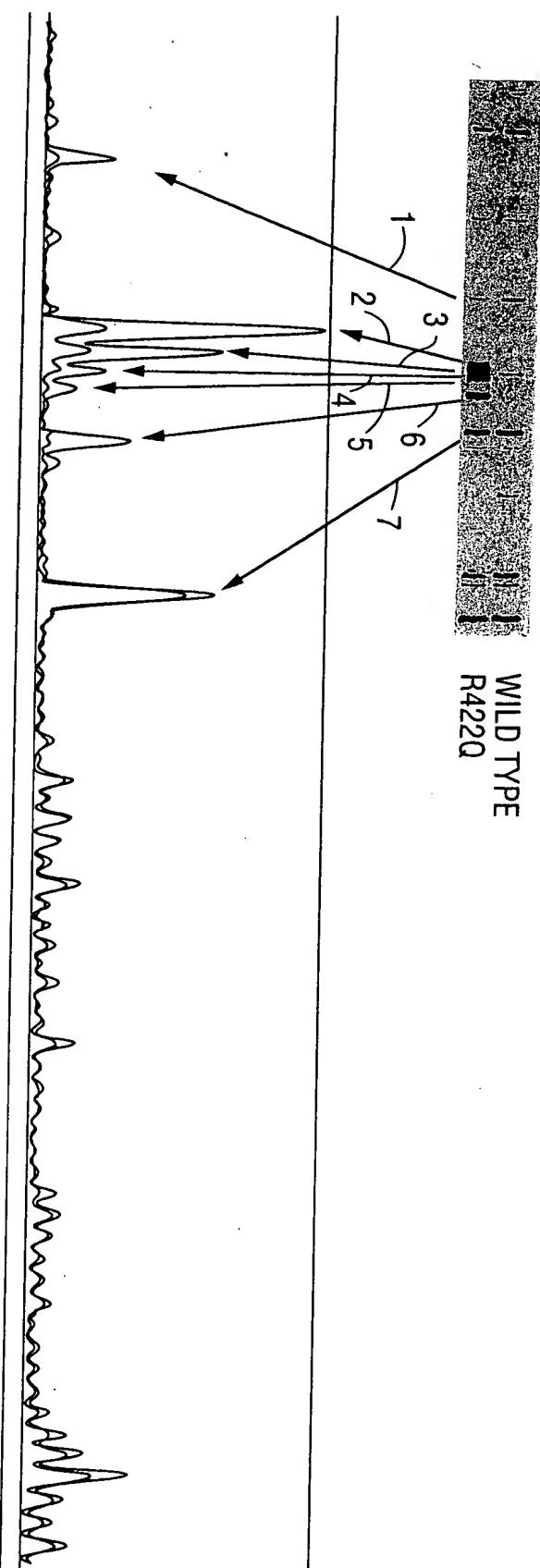


FIG. 48

L:100.8-1 (SEQ ID NO: 76)	5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:46.16-10 (SEQ ID NO: 77)	5' GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:46.16-12 (SEQ ID NO: 78)	5' GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L19.16-3 (SEQ ID NO: 79)	5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:CEM/251 (SEQ ID NO: 80)	5' GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:36.8-3 (SEQ ID NO: 81)	5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC

## "Replacement Sheet"

FIG. 49A

L.100.8-1  
(SEQ ID No: 76)

100  
ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCCGGAACGCCCACTCTCT  
TACAATGCCCTCCATGACCCCTCCTCGCCAGCCCCCTTGCGGTGAGAGA

L.46.16-10  
(SEQ ID No: 77)

ATGTTATGGGAGG-----AGCCGGTCCGGAACACCCACCTTTCT  
TACAATAACCCCTCC-----TCGGCCAGCCCCCTTGCGGTGAAAGA

L.46.16-12  
(SEQ ID No: 78)

ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCC-----TCGGCCAGCCCCCTCCTGGGGAGAGA

L.119.16-3  
(SEQ ID No: 19)

ATGTTACGGGAGGTACTGGGAAGGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCCATGACCCCTCCTGGGGAGAGA

L.CEM/251  
(SEQ ID No: 80)

ATGTTACGGGAGGTACTGGGAAGGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCC-----TCGGCCAGCCCCCTCCTGGGGAGAGA

L.36.8-3  
(SEQ ID No: 81)

ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCCATGACCCCTCCTGGGGAGAGA

"Replacement Sheet"

**FIG. 49B**

L.100.8-1

5' TGATGTATAATATCACTGCATTTGGCTCTGTATTCAAGTCGGCTGGGA  
3' ACTACATTTAGTGAAGCTAAAGGGAGACATAAGTCAGCAGAGCCCT

L.46.16-10

5'-TGATGTATAATATCACCTGCATTCTGCTCTGAAAGCTAGGTAAAGGGAGACATAAGTCAGGAGACCCCT  
3'-ACTACATATTATAGTGA  
CT

L.46.16-12

5' TGGTGTATAATATCACTGCATTGGCTCTGTATTAGCTGGACATAAAGCTAGGAGACCTAAGTCAGGAGACCCCT  
3' ACCACATATTATAGTGA

L.19.16-3

5'-TGATGTATAAATATCACTGCATTGGCTCTGTATTGAGCTTAAAGCAGACATAAAGTCAGGAGACCCCT  
3'-ACTACATATTATAGTGACGTAAAGCAGACATAAAGTCAGGAGACCCCT

L.CEM/251

5' TGATGTATAATAATCAC TGCATT CGCTCTGIA || CAG || G || GGA  
3' ACTACATATTATAAGT GAC GTAAAGCCAGACAT AAGTCAGGAGACCCCT

L.36.8-3

5'-TGATGTATAAATATCACGTGATTGGCTGATGAGACATAAGTCAGGAGACCCCT  
3'-ACTACATATTATAAGTGAACGTAAAGCCGAGACATAAGTCAGGAGACCCCT

## "Replacement Sheet"

FIG. 49C

200  
GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGGAGGTAG  
CTCCGACCCGTCTAACTGGGACCCCTCCAAAGAGGAGGTGATCGTGATCGTCCATC

L. 100. 8-1

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGGAGGTAG  
CTCCGACCCGTCTAACTGGGACCCCTCCAAAGAGGAGGTGATCGTGATCGTCCATC

L. 46. 16-12

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGGAGGTAG  
CTCCGACCCGTCTAACTGGGACCCCTCCAAAGAGGAGGTGATCGTGATCGTCCATC

L. 19. 16-3

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGGAGGTAG  
CTCCGACCCGTCTAACTGGGACCCCTCCAAAGAGGAGGTGATCGTGATCGTCCATC

L. CEM/251

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGGAGGTAG  
CTCCGACCCGTCTAACTGGGACCCCTCCAAAGAGGAGGTGATCGTGATCGTCCATC

L. 36. 8-3

GAGGCTGGCAGATTGAGGCCCTAGGAGGGTTCTCCAGGCACTAGGAGGTAG  
CTCCGACCCGTCTAACTGGGATCCAAAGAGGAGGTGATCGTGATCGTCCATC

"Replacement Sheet"

**FIG. 49D**

L. 100. 8 -1 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTTGGGGTGGG  
(SEQ ID NO: 76) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 46.16-10 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTTGGGG  
(SEQ ID NO: 77) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 46.16-12 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTTGGGG  
(SEQ ID NO: 78) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 19.16-3 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTTGGGG  
(SEQ ID NO: 79) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. CEM/251 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTTGGGG  
(SEQ ID NO: 80) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 36.8-3 5' AGCCTGAGTGGTCCCCCTGCTAAACTCACCAAGGCACCTTTGGGG  
(SEQ ID NO: 81) 3' TCGGACTCACAAAGGACGATTGAGAGTGGTCAACGACCC

HAIRPIN

**FIG. 49E**

300

L. 100. 8 -1  
(SEQ ID No: 76)

L. 46.16-10  
(SEQ ID No: 77)

L. 46.16-12  
(SEQ ID No: 78)

L. 19.16-3  
(SEQ ID No: 79)

L. CEM/251  
(SEQ ID No: 80)

L. 36.8-3  
(SEQ ID No: 81)

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAQCGAGGTGCCGAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAQCGAGGTGCCGAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAQCGAGGTGCCGAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAQCGAGGTGCCGAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAQCGAGGTGCCGAACGAATTTCGAGAAGTTCTGACGGC

CAGAGGCGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCGQCGAGGTGCCGAACGAATTTCGAGAAGTTCTGACGGC

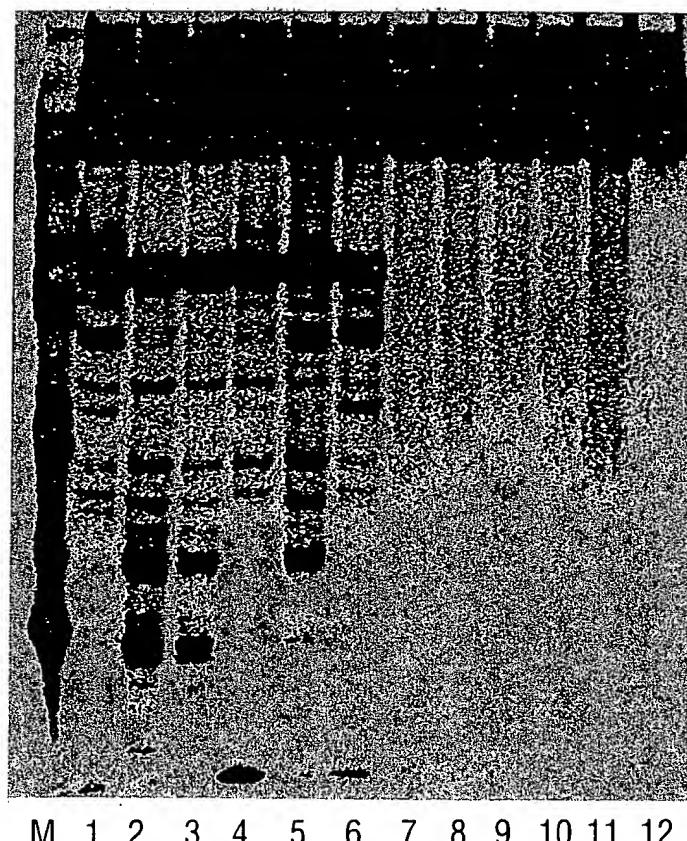
HAIRPIN

FIG. 49F

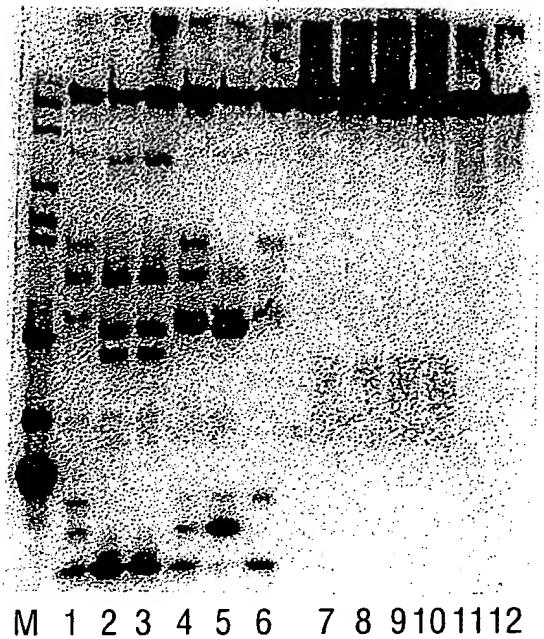
L. 100. 8-1	5' ATT TTAGAAGTAGGCCAGTGTGTTCCCATCTCTCCCTAGCCCCCATCTCTCCCTAGCCCCGCCCCCTG 3' TAAAATCTTCATCCGGTACACACAAGGGTAGAGGGATCGGGGAC	G 3' C 5'
L. 46, 16-10	5' ATT TTAGAAGTAAGCCAGTGTGTTCCCATCTCTCCCTAGCCCCGCCCTG 3' TAAAATCTTCATTGGTCACACACAAGGGTAGAGGGATCGGGGAC	G 3' C 5'
L. 46, 16-12	5' ATT TTAGAAGTAGGGCTAGTGTGTTCCCATCTCTCCCTAGCCCCGCCCTG 3' TAAAATCTTCATCCGGATCACACACAAGGGTAGAGGGATCGGGGAC	G 3' C 5'
L. 19, 16-3	5' ATT TTAGAAGTAAGCTAGTGTGTTCCCATCTCTCCCTAGCCCCGCCCTG 3' TAAAATCTTCATTGGATCACACACAAGGGTAGAGGGATCGGGGAC	G 3' C 5'
L. CEM/251	5' ATT TTAGAAGTAGGGCTAGTGTGTTCCCATCTCTCCCTAGCCCCGCCCTG 3' TAAAATCTTCATCCGGATCACACACAAGGGTAGAGGGATCGGGGAC	G 3' C 5'
L. 36. 8-3	5' ATT TTAGAAGTAGGGCTAGTGTGTTCCCATCTCTCCCTAGCCCCGCCCTG 3' TAAAATCTTCATCCGGATCACACACAAGGGTAGAGGGATCGGGGAC	G 3' C 5'

## "Replacement Sheet"

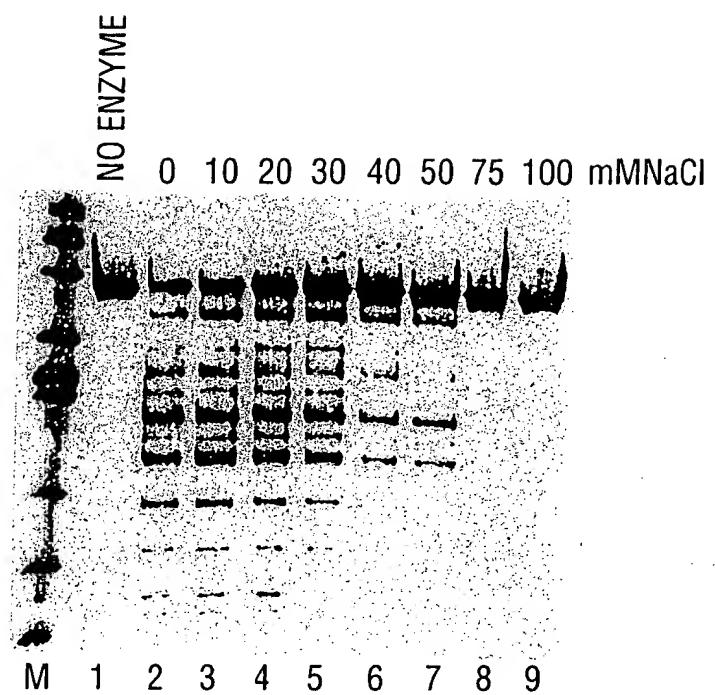
FIG. 49G



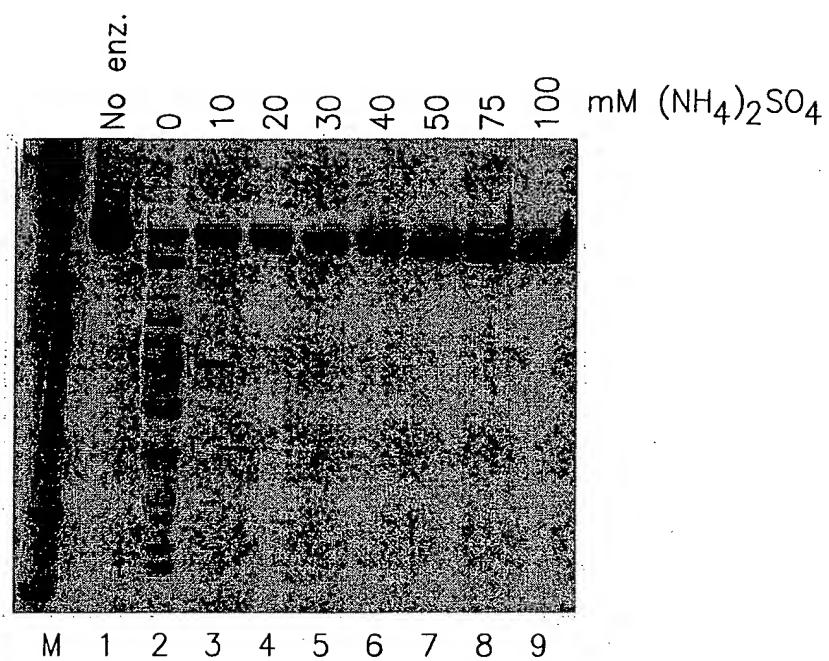
**FIG. 50**



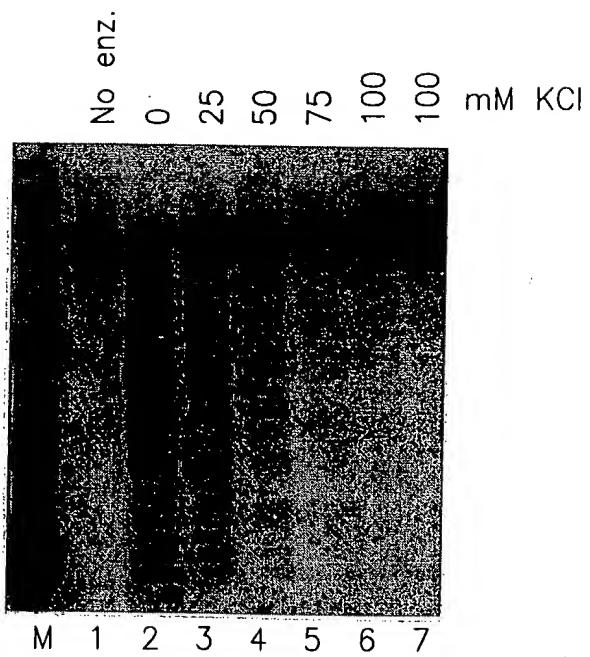
**FIG. 51**



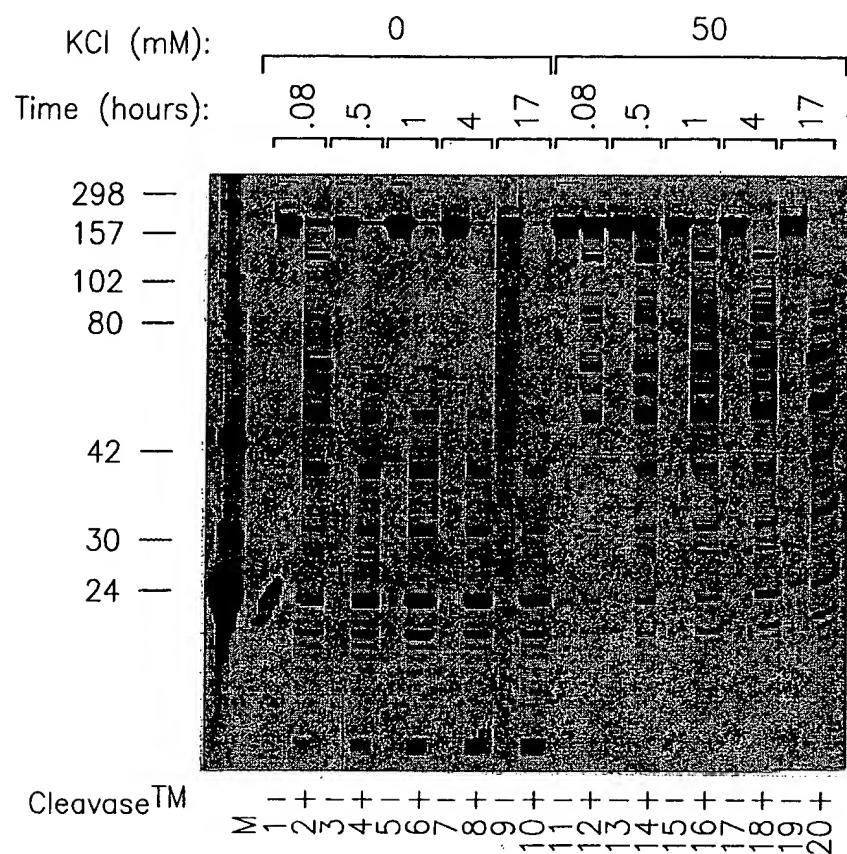
**FIG. 52**



**FIG. 53**



**FIG. 54**



**FIG. 55**

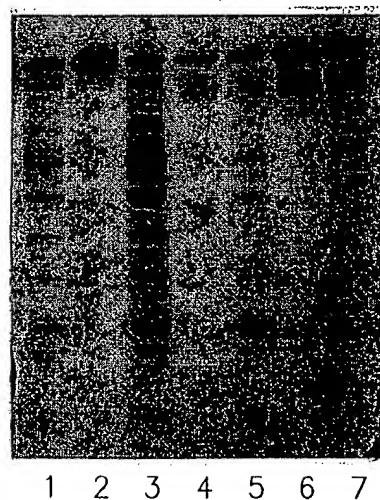
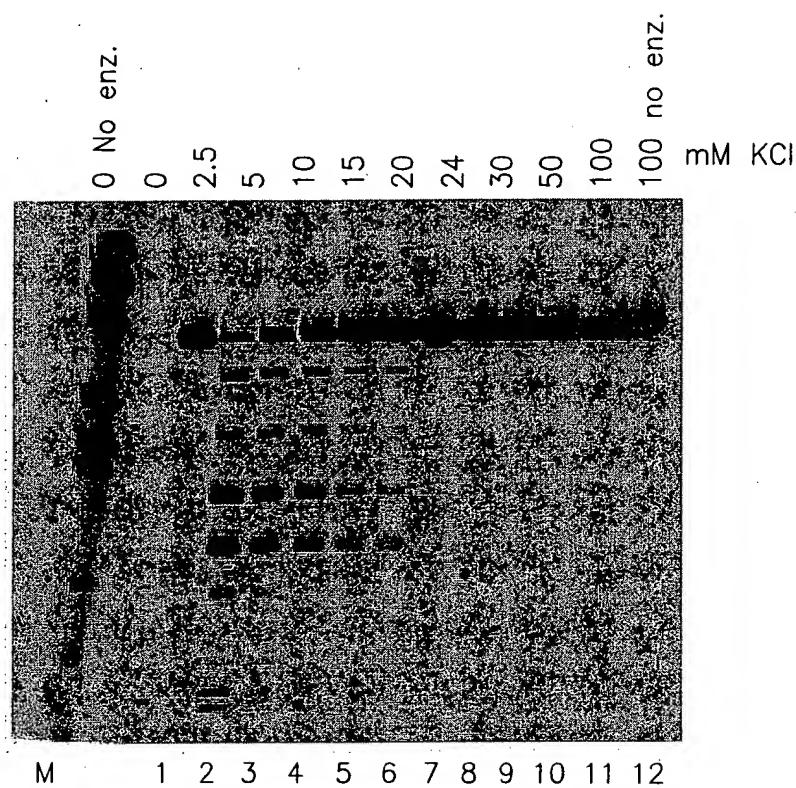
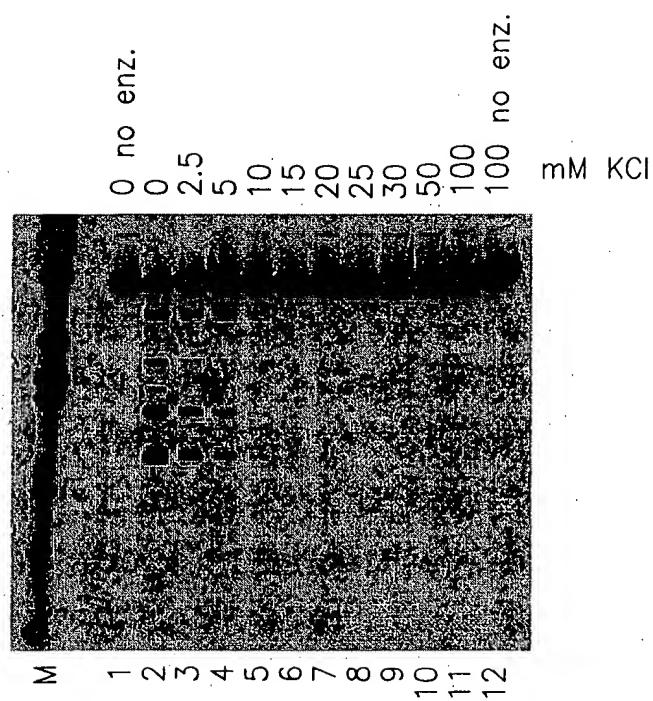


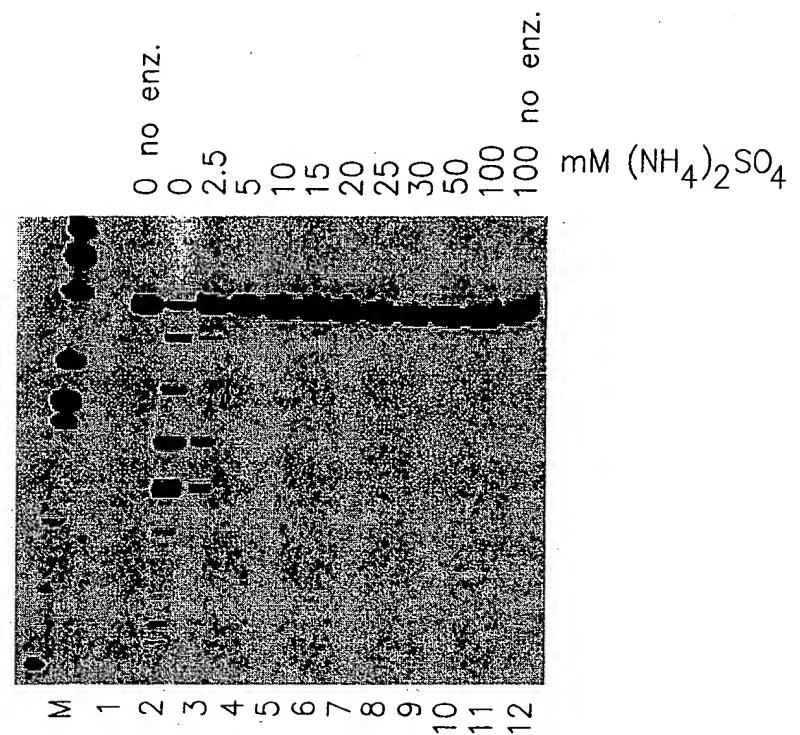
FIG. 56



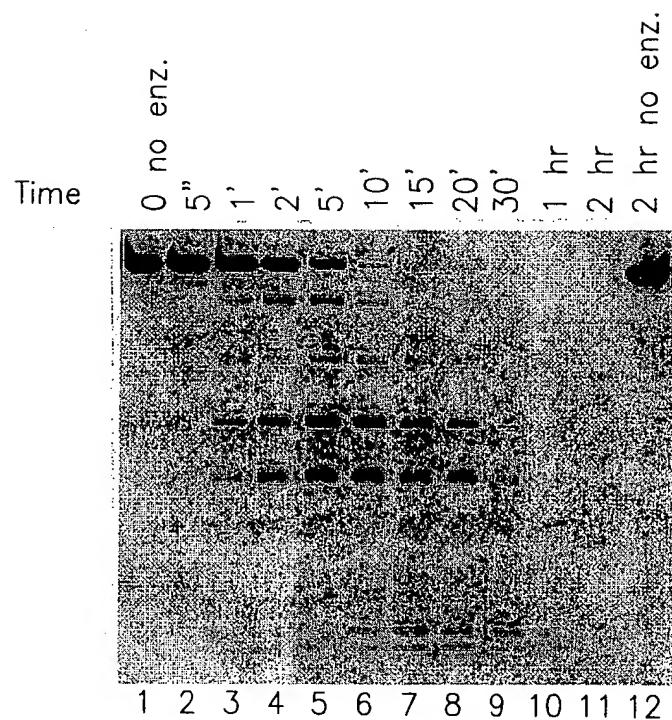
**FIG. 57**



**FIG. 58**

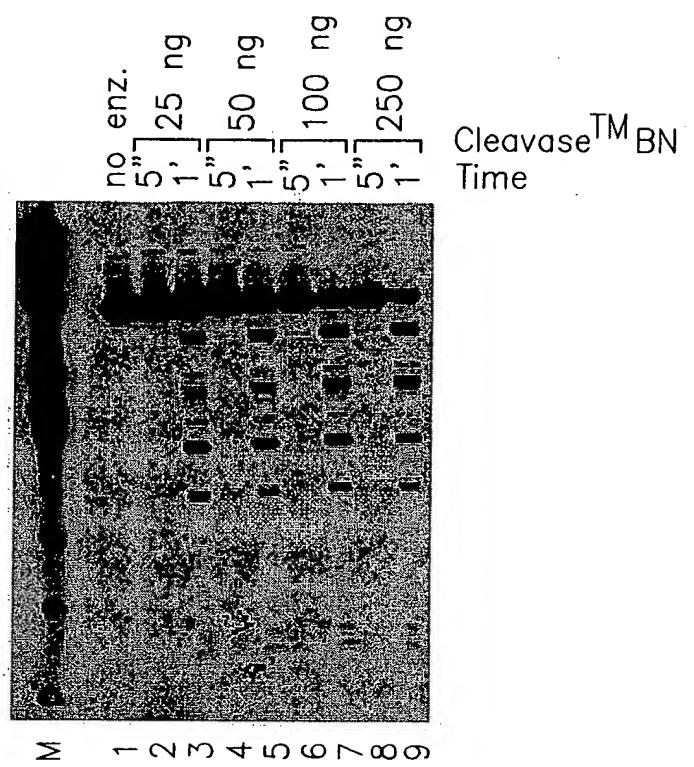


**FIG. 59**



**FIG. 60**

"Replacement Sheet"



**FIG. 61**

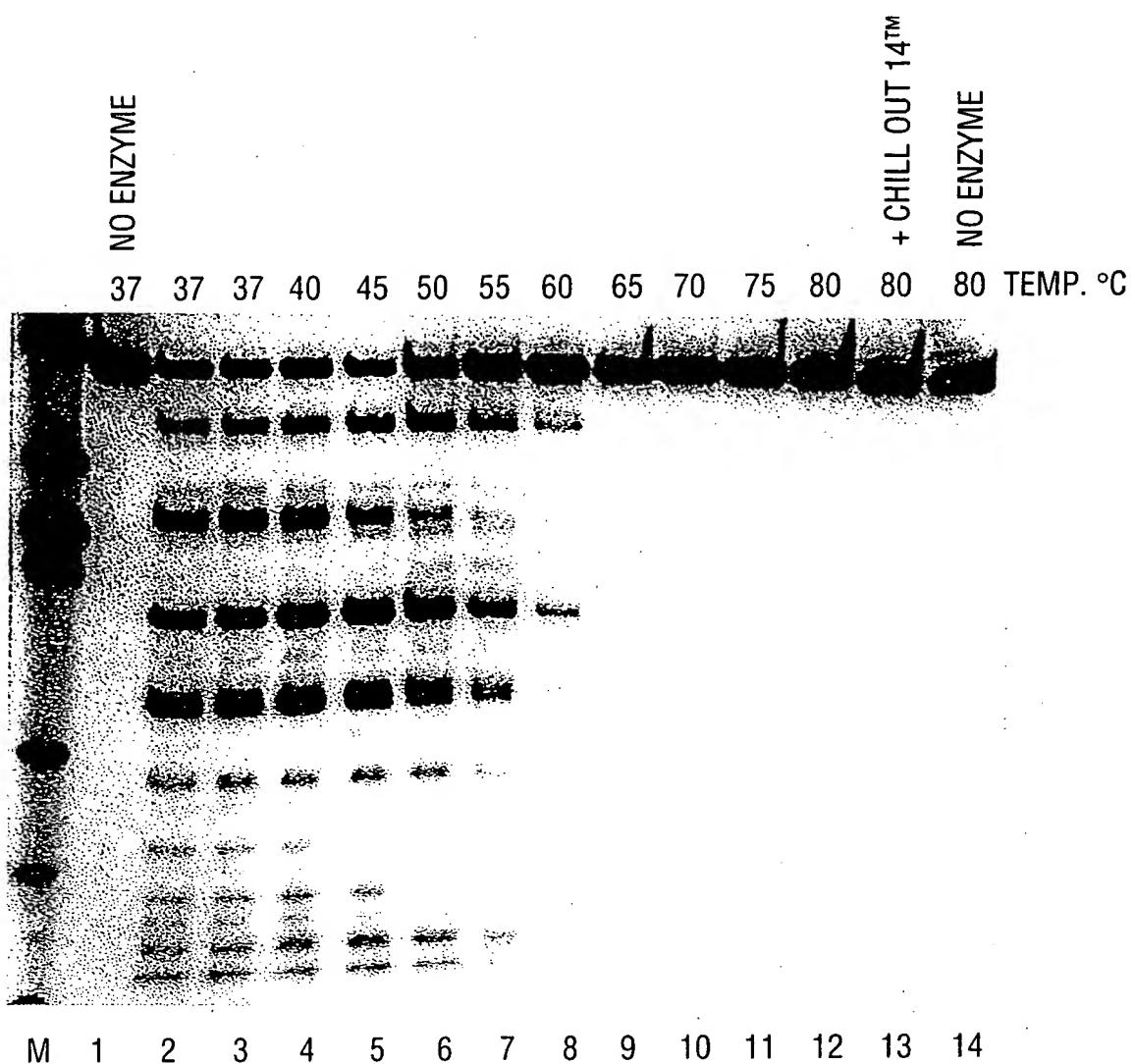
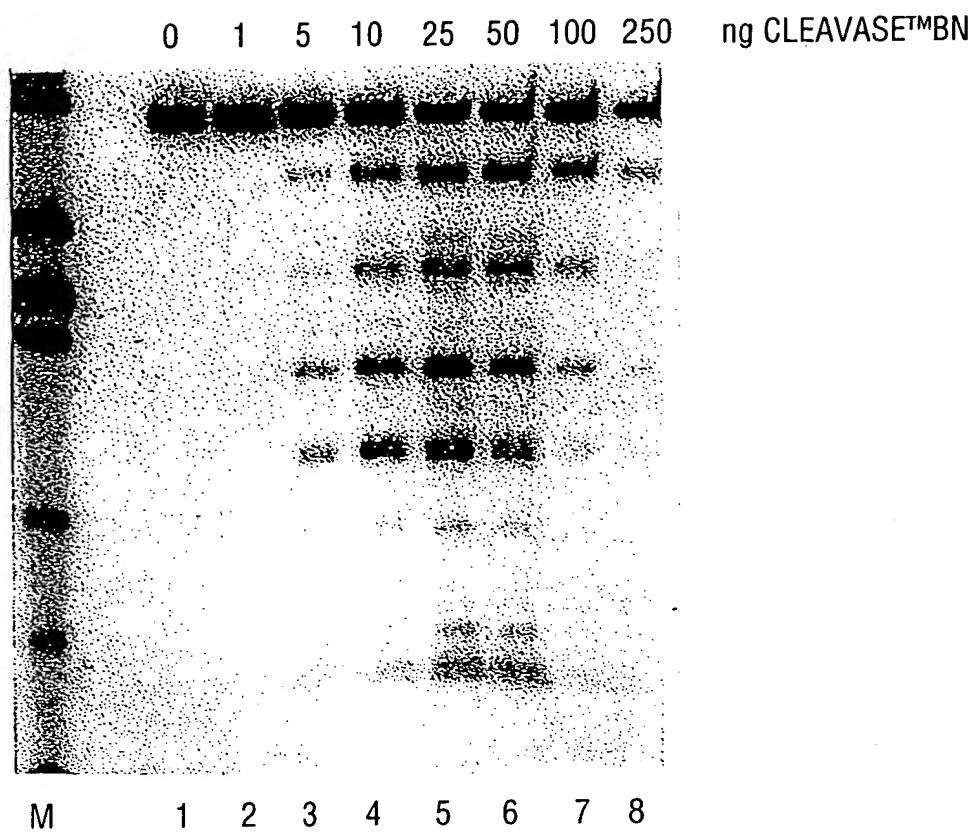
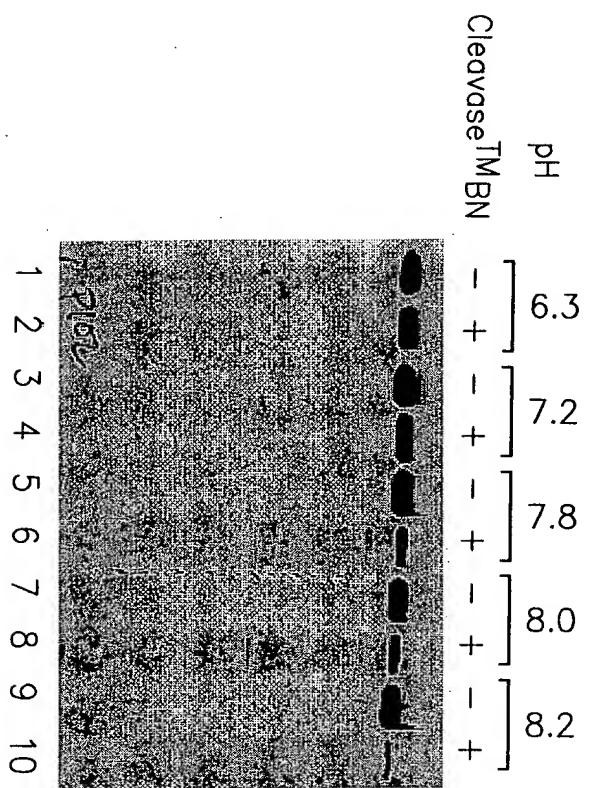


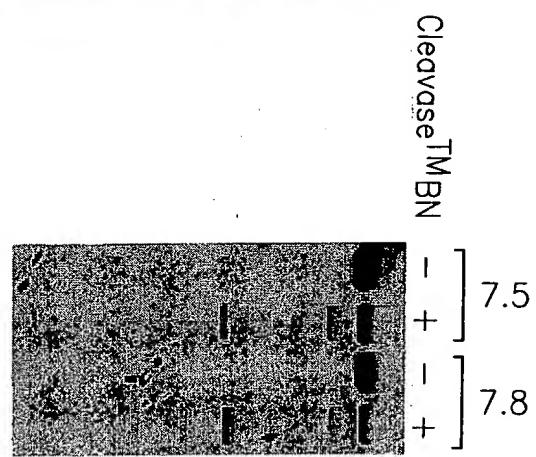
FIG. 62



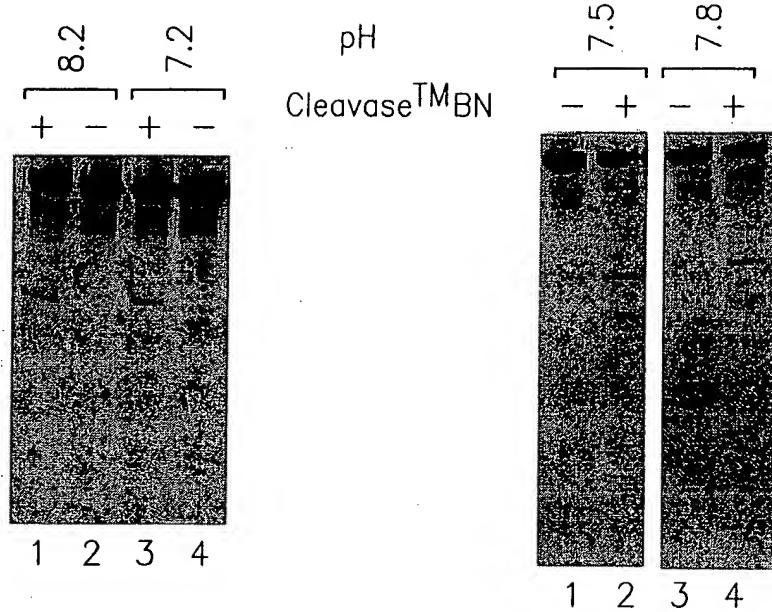
**FIG. 63**



**FIG. 64A**

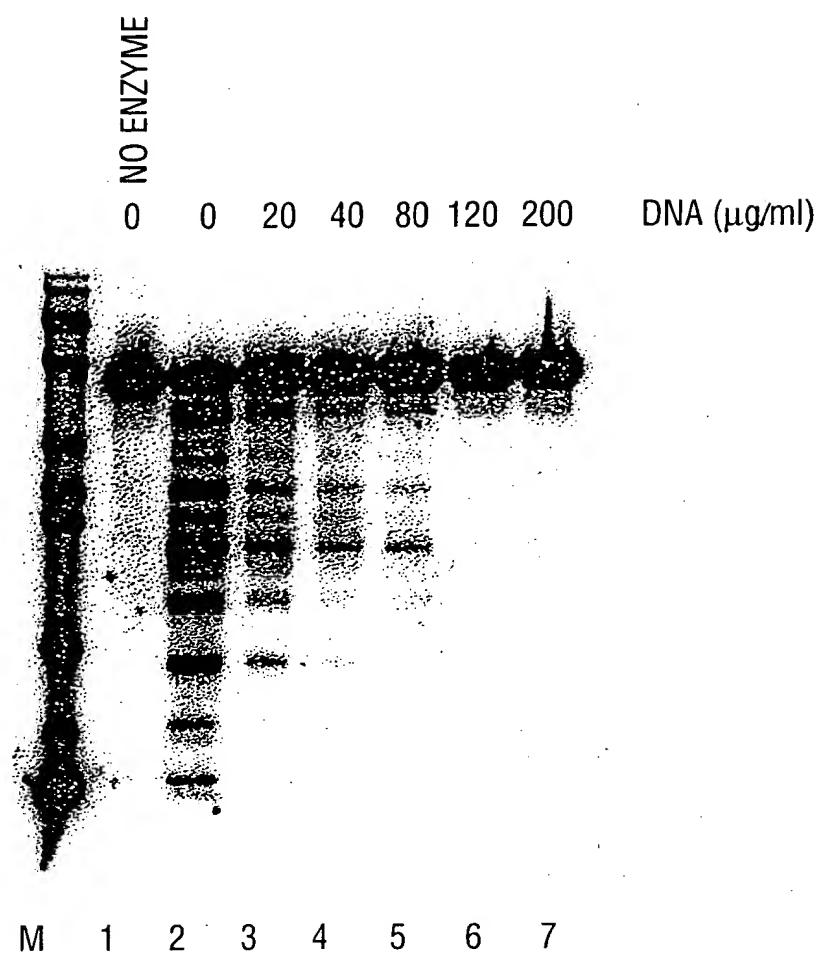


**FIG. 64B**

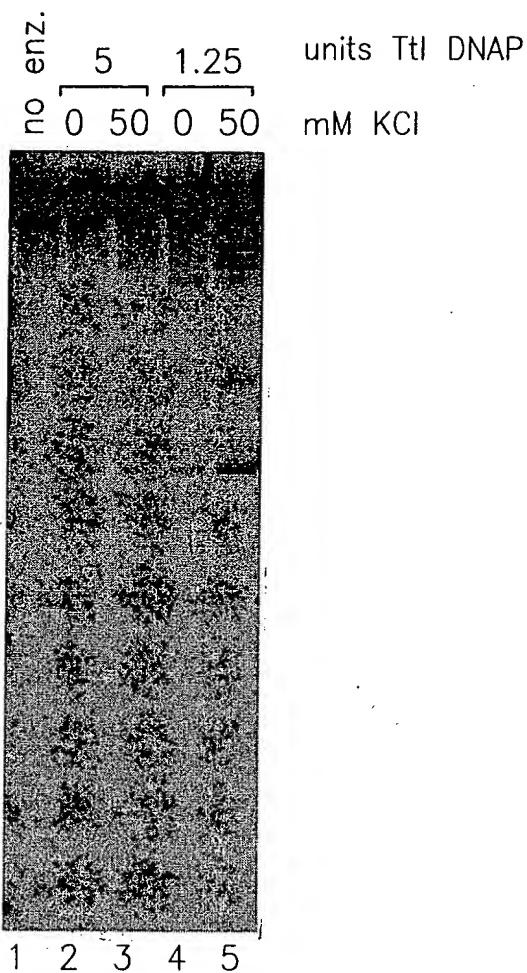


**FIG. 65A**

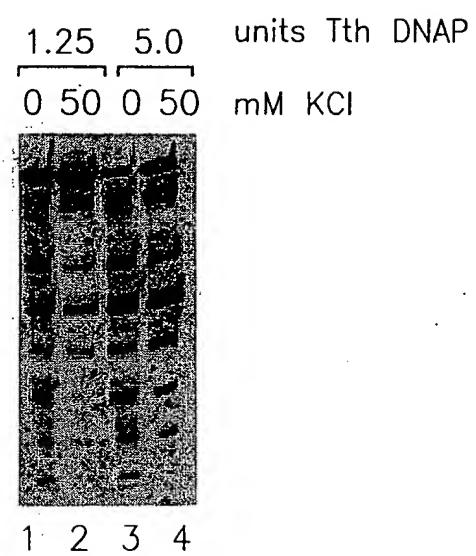
**FIG. 65B**



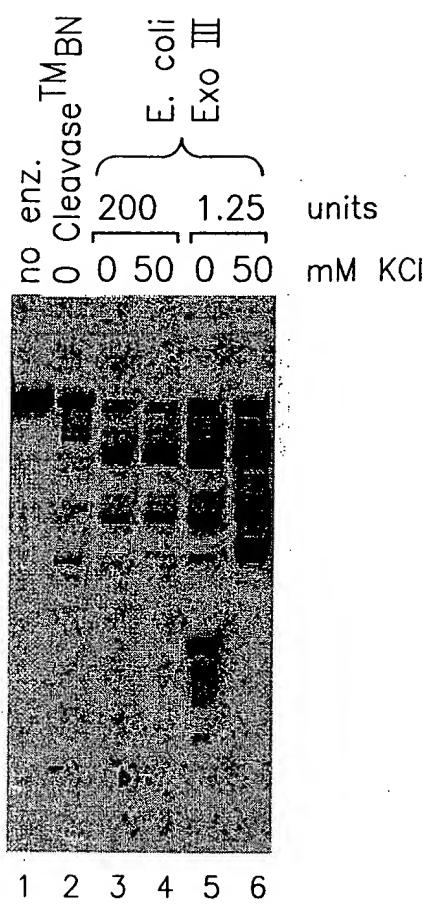
**FIG. 66**



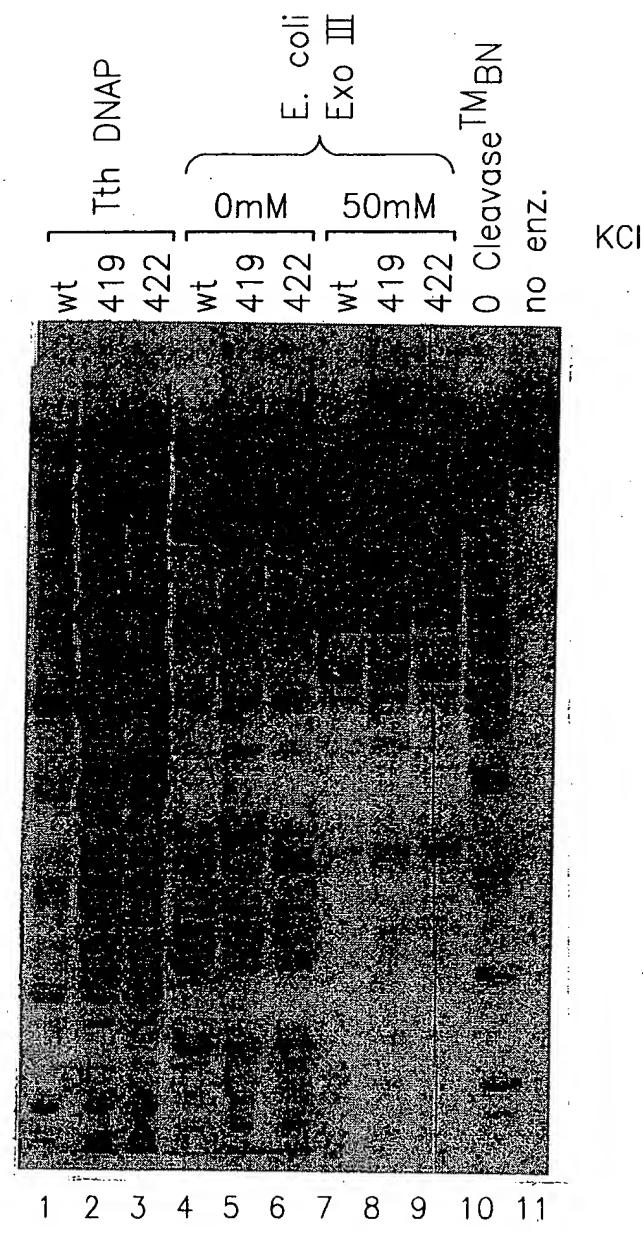
**FIG. 67**



**FIG. 68**

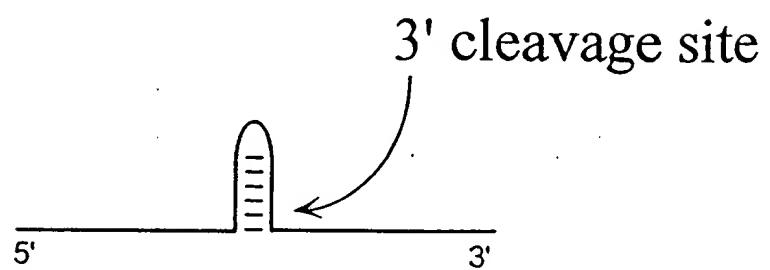
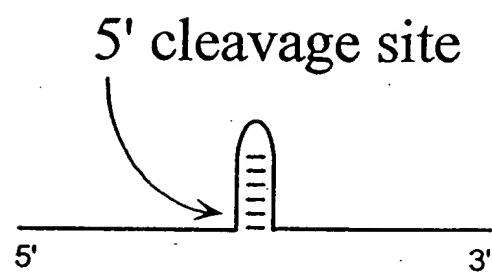


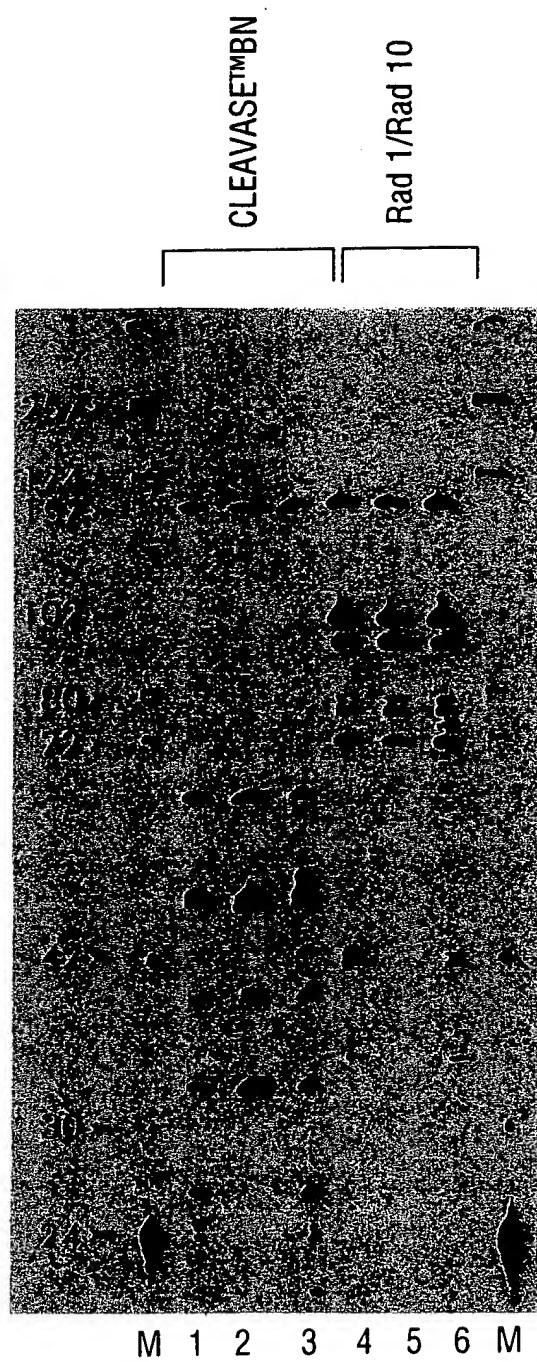
**FIG. 69**



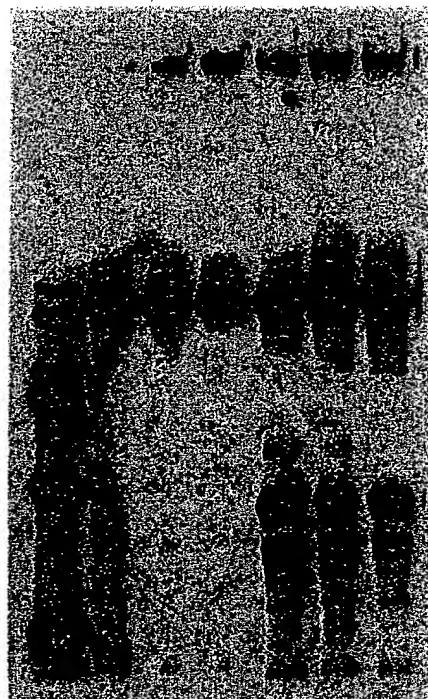
**FIG. 70**

**FIG. 71**





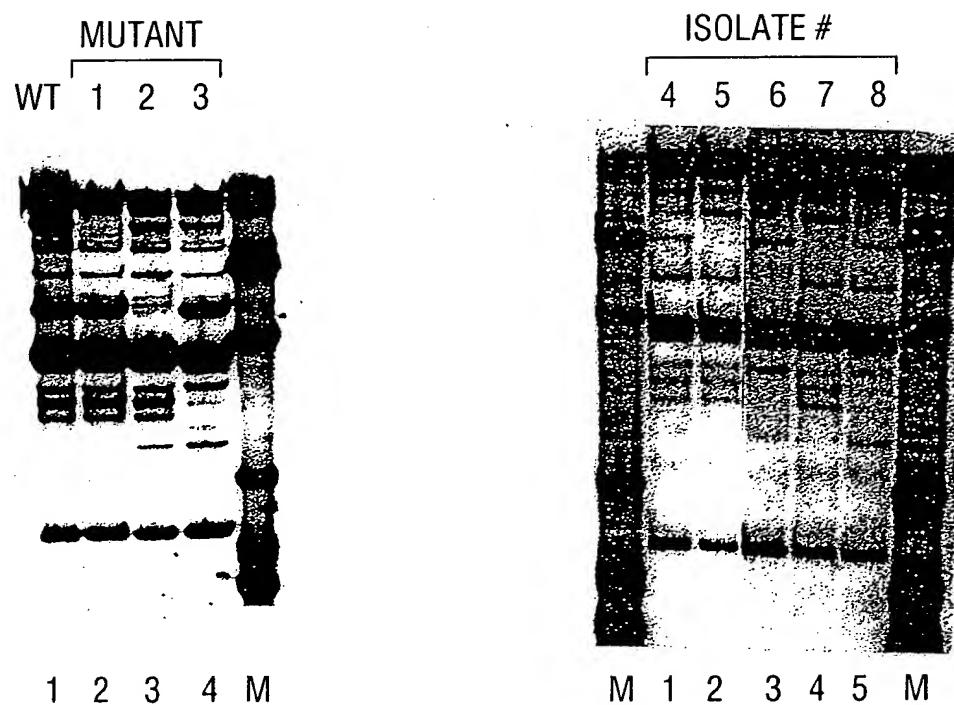
**FIG. 72**



174

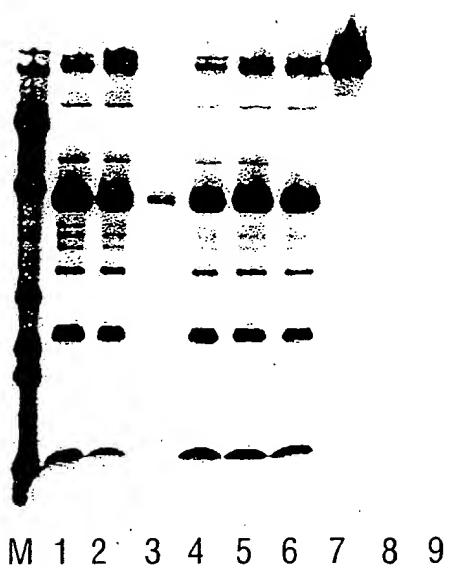
M 1 2 3 4 5 6

**FIG. 73**



**FIG. 74A**

**FIG. 74B**



**FIG. 75**

% OF TOTAL  
MUTATIONS

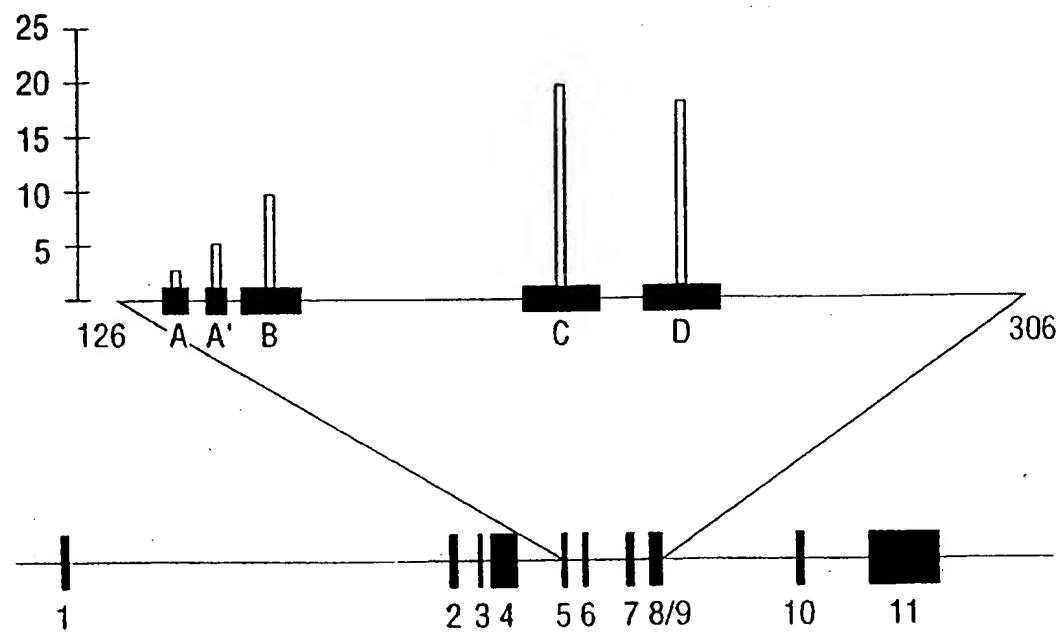


FIG. 76

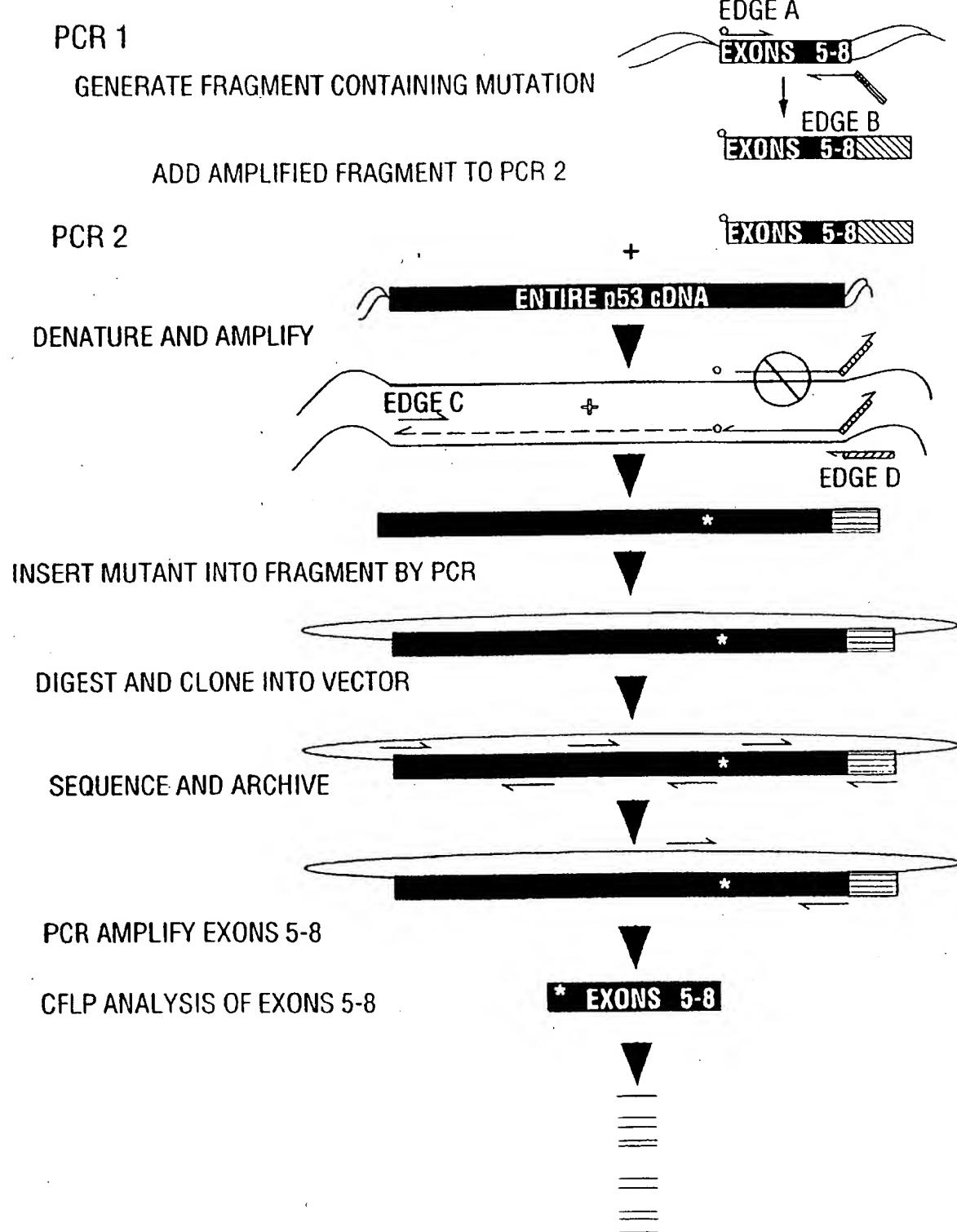
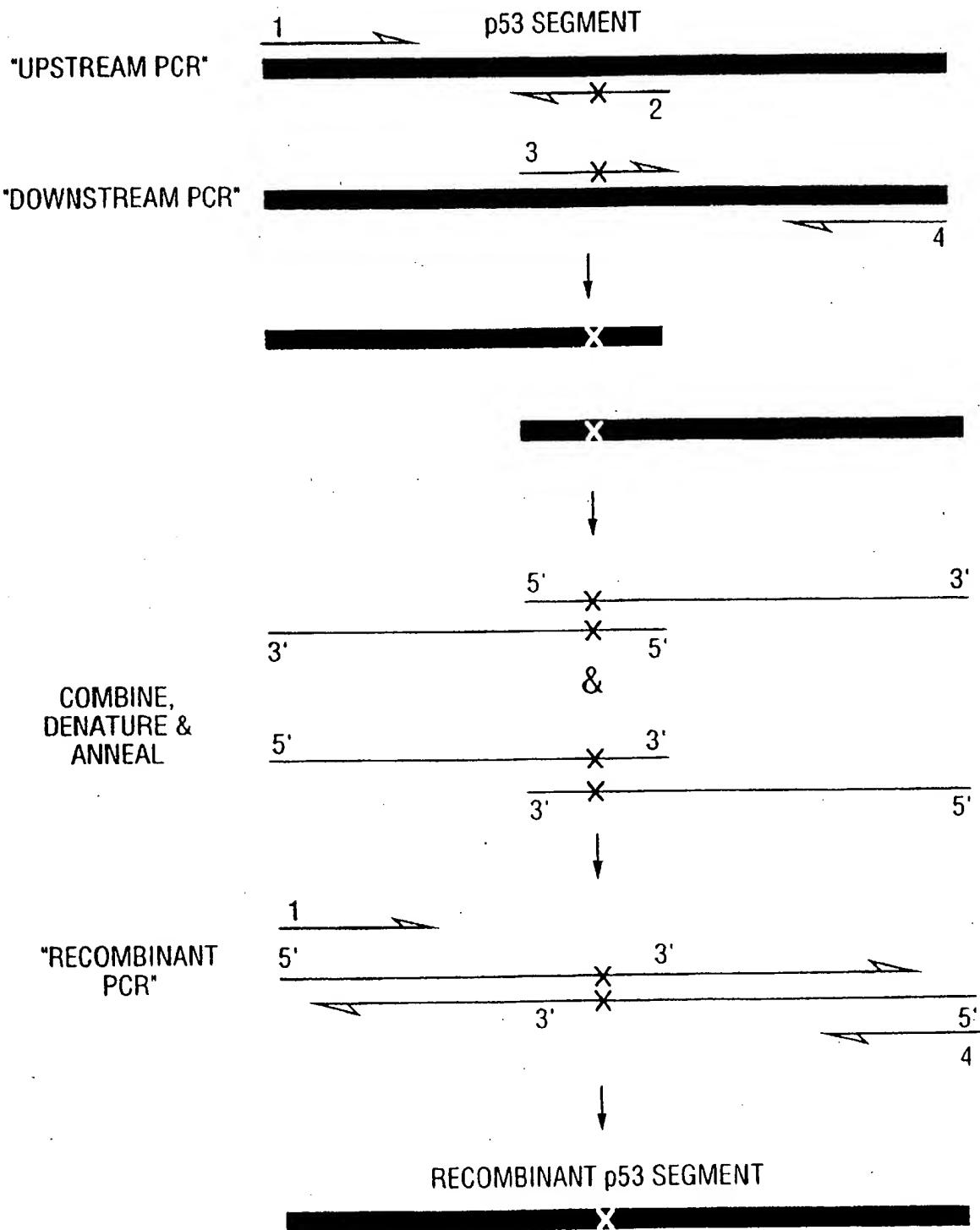
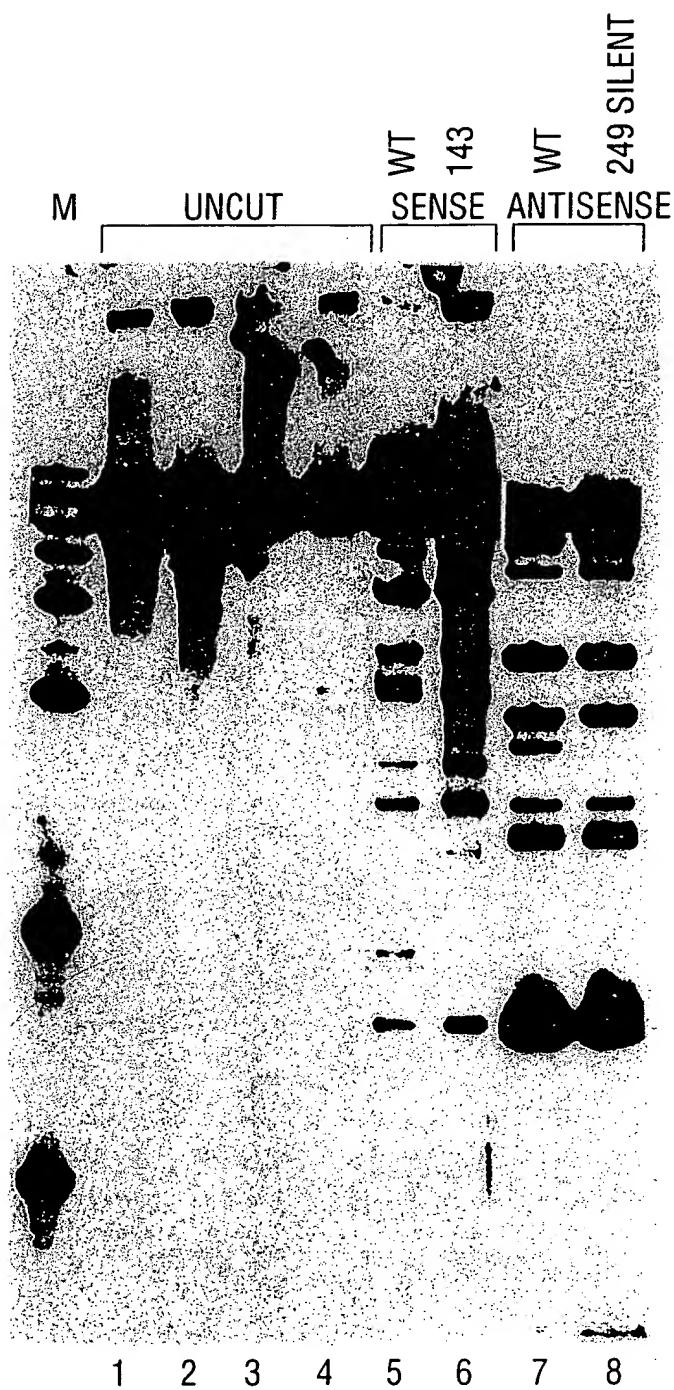


FIG. 77



**FIG. 78**



**FIG. 79**

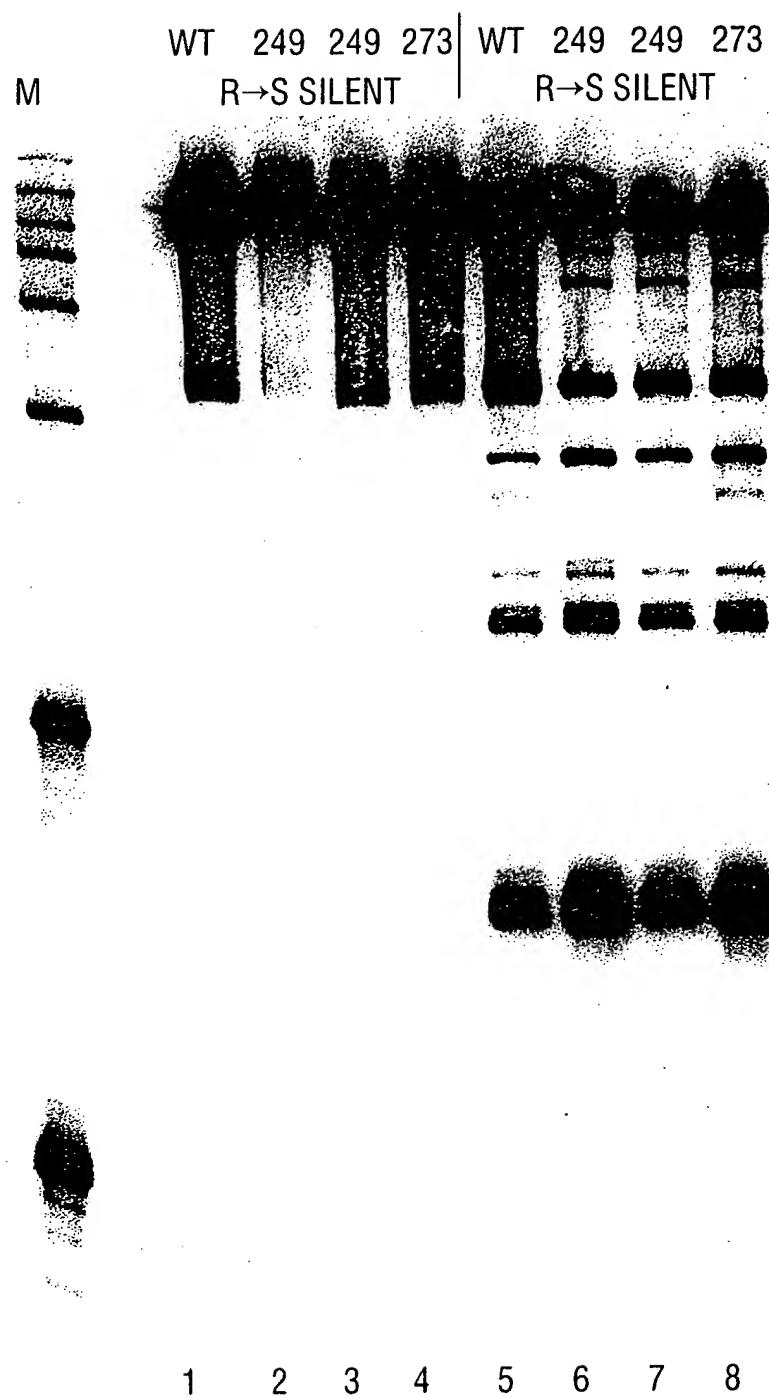


FIG. 80

MIXING PROPORTIONS

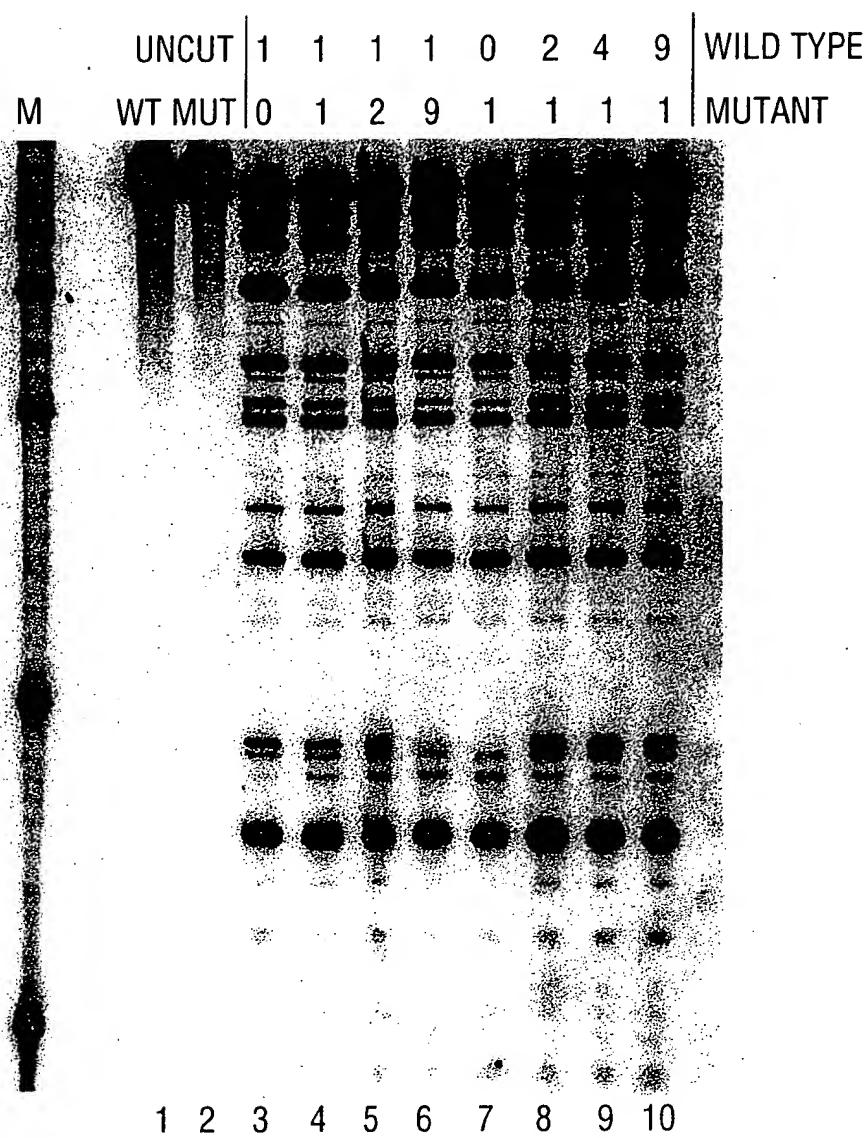


FIG. 81

**FIG. 82**

HCV1.1	(SEQ ID NO:121)	1	CTGCTTCAC	GCAGAAAGCG	TCTGGCCATG	GCCTTAGTAT	GAGTGTGCG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTCAC	GCAGAAAGCG	<u>CCTAGCCATG</u>	GCCTTAGTAT	<u>GAGTGTGCG</u>	
		51	CAGCCTCAG	GACCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1			CAGCCTCAG	GACCCCCCT	CCGGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV2.1			CAGCCTCAG	<u>GT</u> CCCCCT	CCGGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCAG	GACCCCCCT	CCGGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCAG	GACCCCCCT	CCGGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCAG	GCCCCCT	CCGGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCAG	<u>G</u> ACCCCCCT	CCGGGGAGAG	CCATAGTGGT	CTGCGGAACC	
		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT- <u>AAA</u>	100
HCV1.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT- <u>CAA</u>	
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT- <u>CAA</u>	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	<u>GTGGAT</u> <u>GTAA</u>	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCCTTC	<u>GTGGAT</u> <u>GTAA</u>	
HCV6.1			GGTGAGTACA	CCGGAATTGC	<u>CGGGAA</u> ACT	GGGTCCCTTC	<u>TTGGAT</u> - <u>AAA</u>	
HCV7.1			GGTGAGTACA	CCGGAATTGC	<u>TGGG</u> TGACC	GGGTCCCTTC	<u>TGGGAG</u> - <u>CAA</u>	
		151	CCCGCTCAAT	GCCTGGAGAT	TGGGGGTGTC	CCCCGAAAGA	CTGCTAGCCG	150
HCV1.1			CCCGCTCAAT	GCCTGGAGAT	TGGGGGTGTC	CCCCGAAAGA	CTGCTAGCCG	
HCV2.1			CCCGCTCAAT	GCCTGGAGAT	TGGGGGTGTC	CCCCGAAAGA	CTGCTAGCCG	
HCV3.1			CCCGCTCAAT	GCCTGGAGAT	TGGGGGTGTC	CCCCGAAAGA	CTGCTAGCCG	
HCV4.2			CCCGCTCAAT	GCCTGGAGAT	TGGGGGTGTC	CCCCGAAAGA	CTGCTAGCCG	
HCV6.1			CCCGCTCAAT	GCCTGGAGAT	TGGGGGTGTC	CCCCGAAAGA	CTGCTAGCCG	
HCV7.1			CCCGCTCAAT	<u>ACCC</u> <u>CGAA</u> AT	TGGGGGTGTC	CCCCGAAAGA	<u>TCA</u> CTAGCCG	
		201	AGTAGTGTG	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	200
HCV1.1			AGTAGTGTG	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	
HCV2.1			AGTAGTGTG	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	
HCV3.1			AGTAGTGTG	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	
HCV4.2			AGTAGTGTG	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	
HCV6.1			AGTAGGCGT	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	
HCV7.1			AGTAGTGTG	GTCGGGAA	GGCCTTGTGG	TACTGCTGA	TAGGGTGCCT	
		251	GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV1.1			GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV2.1			GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1			GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2			GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1			GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1			GCGAGTGGCC	CGGGAGGTCT	CGTAGACCGT	GC		

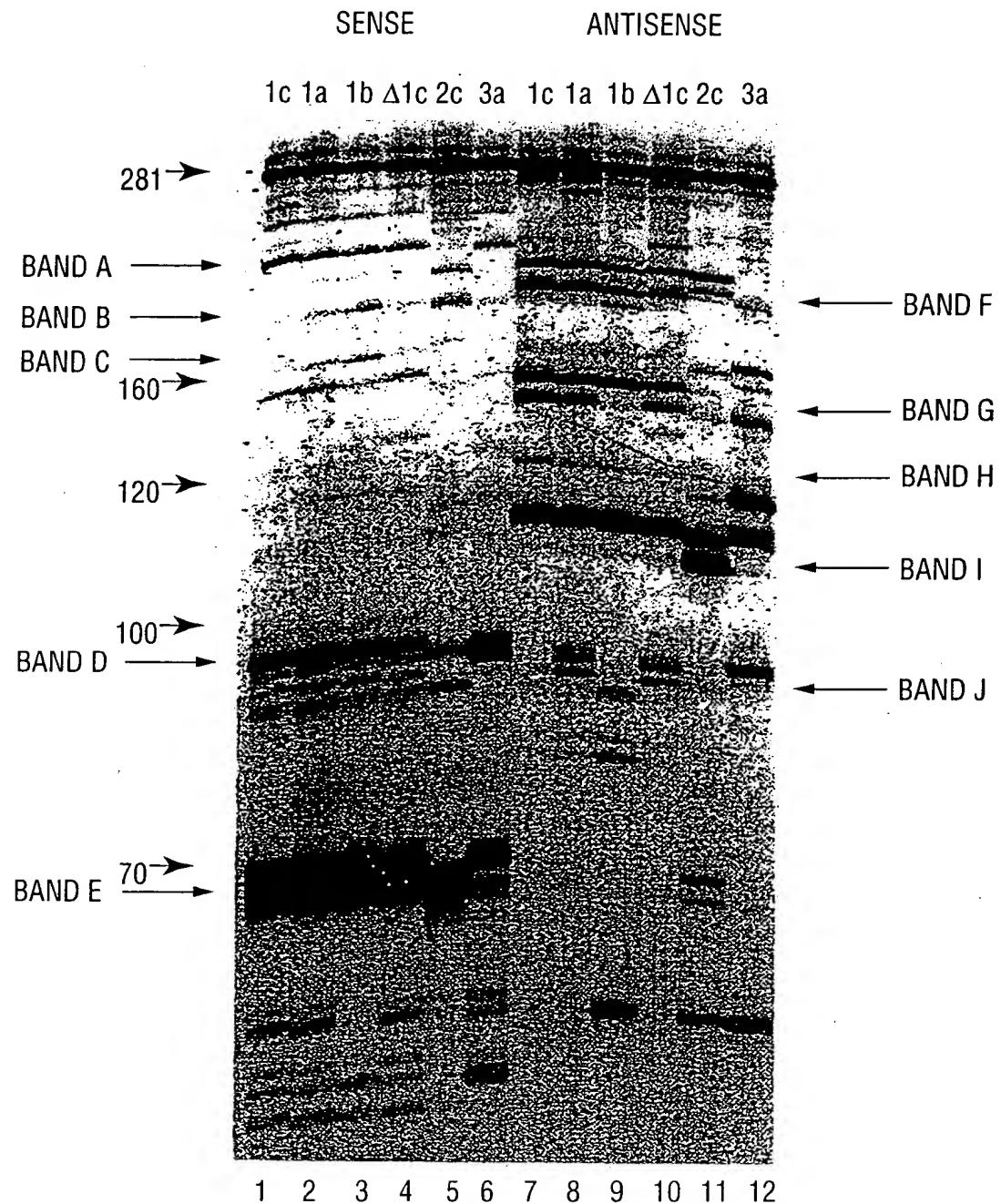


FIG. 83

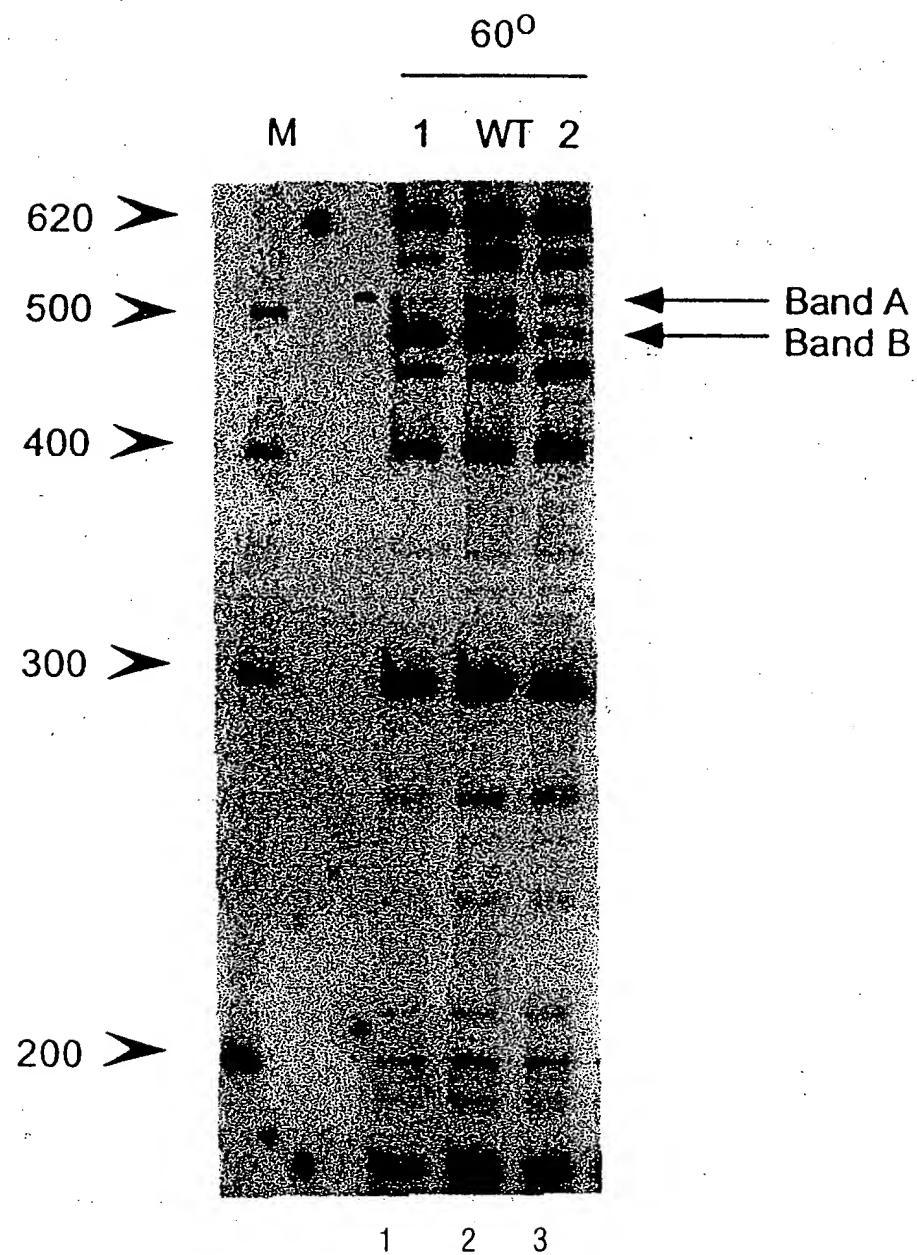


FIG. 84

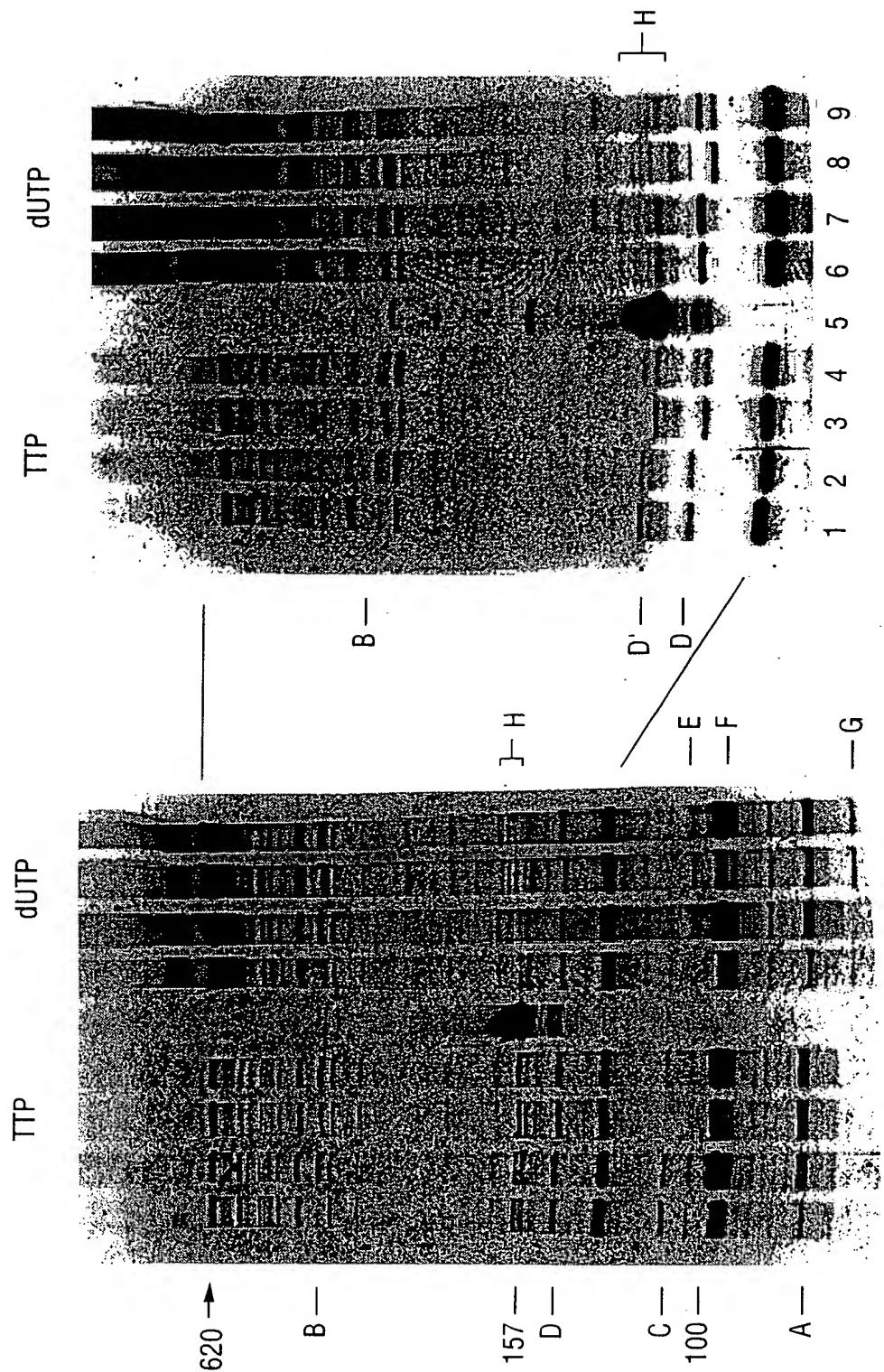


FIG. 85A

FIG. 85B

SENSE STRAND

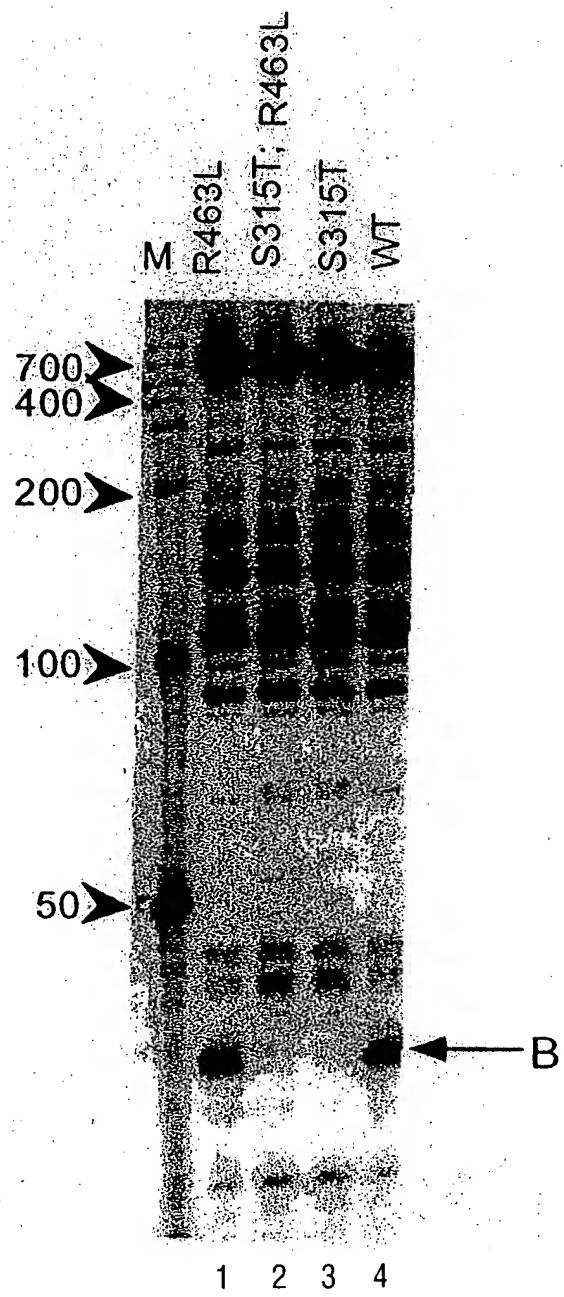
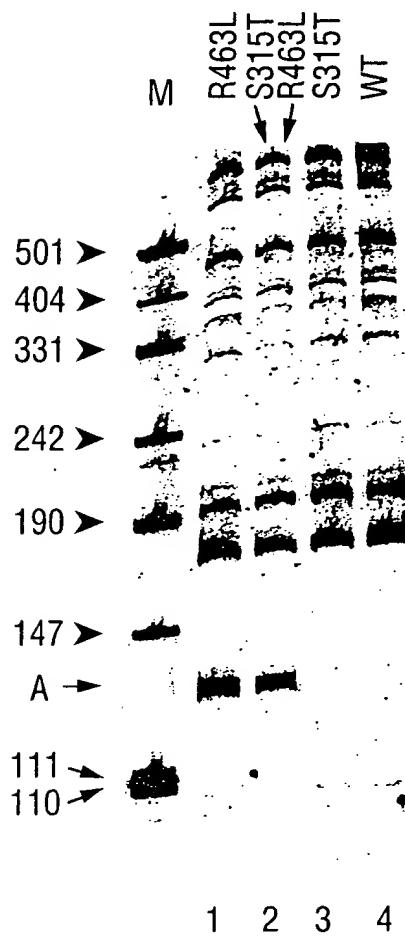


FIG. 86

ANTISENSE STRAND



**FIG. 87**

10	20	30	40	50	60	1638
AGA	GT <del>TTGATC</del> <sub>T</sub> CT	GGCTCAG				
AAATTGAAGA	GT <del>TTGATC</del> <sub>T</sub> AT	GGCTCAGATT	GAACGCTGCC	GGCAGGCCTA	ACACATGCAA	
TTAAC <del>T</del> TCT	CAA <del>ACTAG</del> TAA	CCGAGTCTAA	CTTGCGACCG	CCGTCGGAT	TGTGTACGTT	
70	80	90	100	110	120	ER10
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGGCGGAC	GGGTGAGTAA	
CAGCTTGCCA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	GGGIGAGIAA	
130	140	150	160	170	180	
TGTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCAGATG	
TTGCAGCGTT	CTGGTTCTC	CCCCTGGAAAG	CCCCGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGGGG	TAACGGCTCA	CCTAGGGGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAAGACTCT	
310	320	330	340	350	360	
GGATGACCAAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG	
CCTAATCGAT	GGTGTGACCT	TGACTCTGTG	CCAGGTC <del>TGA</del>	GGATGGCC <del>TCA</del>	GGTCGTCACC	

FIG. 88A

370	380	390	400	410	420
GGAATTTGC	ACAATGGGG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGCCCT
CCTTATAACG					
TGTTACCCGC					
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGGAAGAAG	CACCGGCTAA	CTCCCGTGCCTA	GCAGGCCGGG	TAATACGGAG
CTGCAATGGG					
550	560	570	580	590	600
GGTGCAGCG	TTAATCGGAA	TTACTGGGG	TAAGCCAC	GCAGGGCGTT	TGTTAAGTCA
CCACGGTCCG	AATTAGCCTT	AATGACCCGC	ATTTCGGCGTG	CGTCCGCCAA	ACAATTCACT
610	620	630	640	650	660
GATGTGAAT	CCCCGGGCTC	AACCTGGGA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTA	GGGGCCCGAG		TTGGACCCCT	GACGTAGACT	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAATGCG	TAGAGATCTC	GAGGAATAAC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACGAAGAC	TGACCGCTCAG	GTGGAAAGC	GTGGGGAGCA
CCACCGCTTC	GGGGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

**FIG. 88B**

790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAACGAT	GTCGACTTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCATTTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCCGT	GGCTTCCGGA	GCTAACCGCGT	TAAGTCGACC	GCCTGGGAG	TACGGCCGCA
GAACCTCCGCA	CCGAAGGCCT	CGATTGGCAG	ATTCAAGCTGG	GGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGACCGGGGC	CCGCACAAAGC	GGTGGAGCAT	GTGGTTAAT
TCCAATTTG	AGTTTACTTA	ACTGCCCG	GGCGTGTTCG	CCACCTCGTA	CACCAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GCGGAAGAAC	TTACCTGGTC	TTGACATCCA	CGGAAGTTT	CAGAGATGAG
AGCTACCGTTG	CGCTTCTTGG	AATGGACCAAG	AACTGTAGGT	GCCTTCAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTCCTT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTGCGTCAGCT	CGTGTGTA
TTACACGGAA	GCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
AATGTTGGGT	TAAGTCCCCG	<u>AACGAGCGCA</u>	<u>ACCC</u> TTATCC	TTGTTGCCA	GGGGTCCGGC
TTACAACCCA	ATTCAAGGGCG	TTGCTCGCGT	TTGGAATAGG	AAACAACGGT	GGCCAGGCCG
1150	1160	1170	1180	1190	1200
CGGGAACCTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC
GGCCTTGAGT	TTCTCTGAC	GGTCACTATT	TGACCTCCCT	CCACCCCTAC	TGCAAGTTCAG

SB-1

SB-3

SB-4

**FIG. 88C**

1210	1220	1230	1240	1250	1260
ATCATGGCC	TTA				
ATCATGGCC	TTACGA				
<u>ATCATGGCC</u>	<u>TTACG</u> <u>ACCAG</u>	<u>GGCTACACAC</u>	<u>GTGCTACA</u>	<u>GGCGCATACA</u>	<u>AAGAGAAGCG</u>
TAGTACCGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGGTATGT	TTCTCTCGC
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTCGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAAC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAGTCCGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT
AGCTGAGGT	CTTCAGCCTT	AGGGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACTTATGCA</u>
			GC	CACTTATGCA	
1390	1400	1410	1420	1430	1440
TCCCGGGCT	TGTACACACC	GCCCCGTCA	CCATGGGGAGT	GGGTTGCAA	AGAAGTAGGT
<u>AGGGCCCGGA</u>	<u>ACATGTGTGG</u>	<u>CGGGCAGTGT</u>	<u>GGTACCCCTCA</u>	<u>CCCAAACGTTT</u>	<u>TCTTCATCCA</u>
AGGGCCCGGA	ACATG				
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA
TCGAATTGGA	AGCCCTCCCC	CGAATGGTGA	AACACTAAGT	ACTGACCCCC	CTTCAGCATT
1510	1520	1530	1540	1550	
CAAGGTTAAC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCCTTG	GACGCCAAC	TAGTGGAGGA	AT.....	

SB-3  
SB-4

1743

**FIG. 88D**

1638 (SEQ ID NO:151) AGAGTTGATCCTGGCTCAG  
 E.colirrSE (SEQ ID NO:158) 0 :.AAATTGAAAGAGTTGATCAGGCTCAGATTGAACGGCTGGGGCAGGCCAACATGCA  
 Cam.jejuns (SEQ ID NO:159) 0 .TTTTATGGAGTTGATCCTGGCTCAGAGTGAACGGCTGGGGGCTAATACATGCA  
 Stp.aureus (SEQ ID NO:160) 0 .TTTTATGGAGTTGATCCTGGCTCAGGATGAACGGCTGGGGGCTAATACATGCA

ER10 (SEQ ID NO:152) 60 AGTCGAACGGTAACAG----GAAGAAAGCTTGGCTCTT----GCTGACGAGTGGGGGACGGG  
 E.colirrSE 62 AGTCGAACGGAT----GAAGCTCTAGCTGGCTAGAAGTGG----TTAGTGGGGCACGGG  
 Cam.jejuns 61 AGTCGAACGGAA----GGGACGAGAAGCTTGGCTCTGATG----TTAGGGGGGACGGG

ER10 114 TGAGTAA  
 E.colirrSE 114 TGAGTAATGCTGGGA-ACTGCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATA  
 Cam.jejuns 114 TGAGTAAGGTATAGTTAACCTGCCCCAACAGAGGACAAACAGTTGGAACAGACTGCTAATA  
 Stp.aureus 113 TGAGTAACACGGTGGATAACCTACCTATAAGACTGGGATAACTTGGGAAACGGGAGCTAATA

E.colirrSE 175 CCGCATAAC----GTCGCAAGAC----CAAAGAGGGGACCTTCG-GGCGCTCTG  
 Cam.jejuns 176 CTCTTAACGGTGGCTAACACAAGTGGTAGG-GAAAG----TTTT----CG  
 Stp.aureus 175 CCGGATAATATTTGAACCGCATGGTCAAAGTGAAGACGGGT----CTT----GCTGTCA

E.colirrSE 221 CCATGGGATGTGCCAGATGGGATTAGCTAGTAGGGGGTAACGGCTCACCTAGGGGACGA  
 Cam.jejuns 221 GTGTAGGGATGAGACTATAAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGGTATGA  
 Stp.aureus 229 CTTATAGATGGATCCGGCCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirrSE 283 TCCCTAGCTGGTCTGAGAGGGATGACCACACTGGGAACTGAGACACGGTCCAGACTCCTA  
 Cam.jejuns 283 CGCTTAACGGTCTGAGAGGGATGACTCAGTCACACTGGGAACTGAGACACGGTCCAGACTCCTA  
 Stp.aureus 291 TACGTAGCCGACCTGAGAGGGTGATGGCACACTGGGAACTGAGACACGGTCCAGACTCCTA  
 1659 (COMPL) ACTCCTA

FIG. 89A

E.colirrSE  
Cam.jejun5  
Stp.aureus  
1659 (COMPL)

345 CGGGAGGCAGCTGGGAATTTGACAAATGGGCCAAGCCTGATGCCAGCCATGCCCGCTG  
345 CGGGAGGCAGCTGGGAATTTGACAAATGGGCCAATGGGAAACCTGACGCCAGCACGCCCGCTG  
353 CGGGAGGCAGCTGGGAATTTGCCAATGGGCCAAGCCTGACGGAGCACGCCCGCTG  
CGGGAGGCAGCAG

E.colirrSE  
Cam.jejun5  
Stp.aureus

407 TATGAAAGAAGGCCCTCGGTTGTAAGTACTTCAGCGGGAGGAA-GGGACTAAAGTAA  
407 GAGGATGACACTTTGGAGCGTAACCTCTTCTTAGGGAAAG-----AATT  
415 AGTGATGAAGGTCTCGGATCGTAAACTCTGTATTAGGGAAAGAACATATGTGTAAGTAAC

E.colirrSE  
Cam.jejun5  
Stp.aureus

468 ACCTTTGCTCATTGACGTTACCCGAGAAGAACCGGCTAACTCCGTGCCAGGCCCG  
455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGGCCCG  
476 -----TGTCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGGCCCG

FIG. 89B

"Replacement Sheet"

E. coli rrSE	530	GTAATACGGAGGGTGC
Cam. jejun5	506	GTAATACGGAGGGTGC
Stp. aureus	538	GTAAATACGGTAGGTGGCAAGCGTTATCGGAATT
E. coli rrSE	592	GTTAAGTCAGATGTGA
Cam. jejun5	568	ATCAAGTCTTGTGA
Stp. aureus	600	TTAAGTCTGATGTGA
E. coli rrSE	654	GAGTCTCGTAGAGGGGGT
Cam. jejun5	630	GAGTGAGGGAGAGGC
Stp. aureus	662	GAGTGCAGAAGAGGA
E. coli rrSE	716	ATACCGGTGGCGAAGGC
Cam. jejun5	692	ATACCCATTGCGAAGGCC
Stp. aureus	724	ACACCAAGTGGCGAAC
E. coli rrSE	778	GCAACAGGATTAGATAC
Cam. jejun5	754	GCAACAGGATTAGATAC
Stp. aureus	786	TCAAACAGGATTAGATAC

FIG. 89C

"Replacement Sheet"

E. coli rrSE	840	C- <u>CTTGA</u> -GGGTGGCTCCGGAGCTAACGGGTTAACGGCTGACCCCTGGGGACTACGGCC
Cam. jejun5	816	G- <u>CTAGT</u> -CATCTCA <del>GT</del> TAATGCAGCTAACGGATTAAGTGTACCCCTGGGAGTACGGTCGC
Stp. aureus	848	GT- <u>TTCCG</u> CCCTTAGTGCTGCAGCTAACGGCTAACGCACTCCGCTGGGAGTACGACCGC
E. coli rrSE	900	AAGGTTAAACTCAAATGAATTGACGGGGCCGACAAAGCGGTGGACATGTGGTTAATT
Cam. jejun5	876	AAGGTTAAACTCAAAGGAATAGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Stp. aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTAATT
E. coli rrSE	962	CGATGCAACGGCGAACCTTACCTGGTCTTGACATCCACGGAGTTTCAGAGATGAGAAT
Cam. jejun5	938	CGAAGATAGCGCGAACCTTACCTGGGCTTATCTTAAGAACCTTTAGAGATAAGAGG
Stp. aureus	971	CGAAGCAACGCCAACCTTACCAAATCTTGACATCCTTGACAACACTCTAGAGATAGAGCC
E. coli rrSE	1024	GTG- <u>CCTTCGGG</u> -AA-CGGTGAGACAGGTGCTGCATGGCTGTCAGCTCGTGTGTA
Cam. jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGGTGCACGGCTGTCAGCTCGTGTGTA
Stp. aureus	1033	TTCC- <u>CCTCGGG</u> -GGACAAAGTGACAGGGTGGTCATGGTTGTCAGCTCGTGTGTA
SB-1		GCACCGAGCCAAACCC
E. coli rrSE	1081	AATGTTGGGTTAACGTCGGCAACGGCGAACCCCTTATCCTTGTGCAGCGGTCCGG-CC
Cam. jejun5	1061	GATGTTGGGTTAACGTCGGCAACGGAGCGAACCCACGGTATTAGTTGCTAACGGTTGG-CC
Stp. aureus	1092	GATGTTGGGTTAACGTCGGCAACGGAGCGAACCCCTTAAGCTTAGTTGCTAACGCA- <u>TTAAGT</u> -T

FIG. 89D

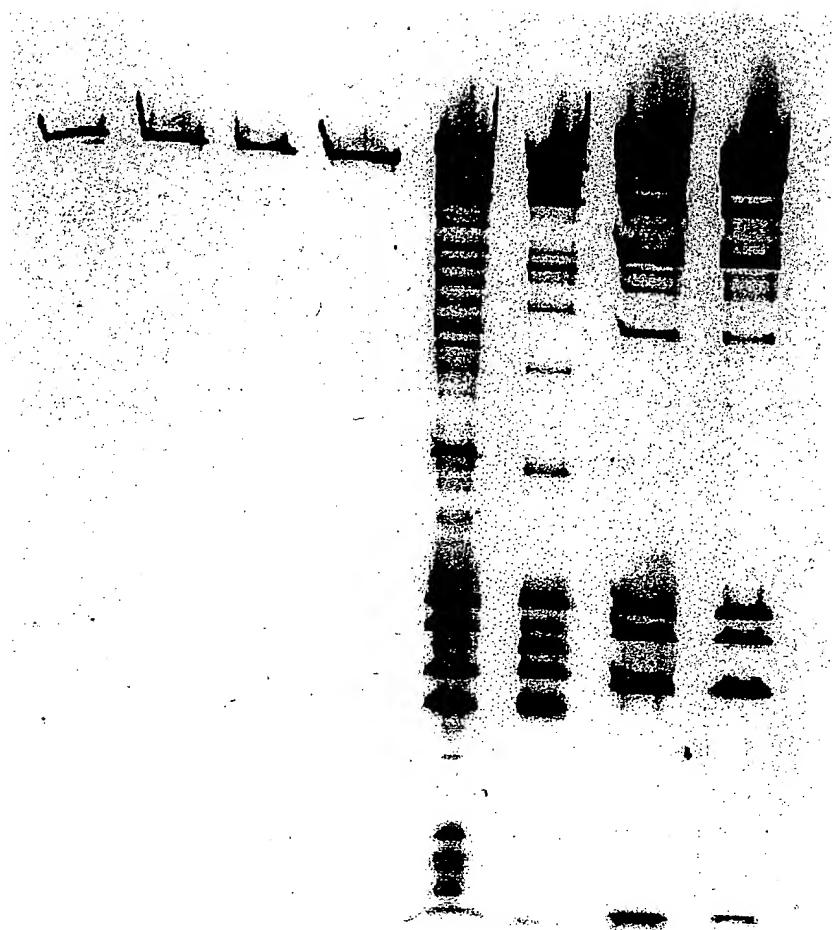
SB-3	(SEQ ID NO:157)	ATGACGTCAGTCATC
SB-4	(SEQ ID NO:154)	ATGACGTCAGTCATC
E.colirrSE	1142 GGGAACTCAAAGGAGACTGGCAGTGATAACTGGAGGAAGGTGGGGATGACGTCAGTCATC	
Cam.jejunS	1122 GAGCACTCTAAATAGACTGCCCTCG-TAAGGAGGAGGAAGGTGGGACGACGTCAGTCATC	
Stp.aureus	1152 GGGCACTCTAAGTGTACTGCCGGTACAACGGAGGAGGTGGGATGACGTCAGTCATC	
SB-3	ATGGCCCTTA	
SB-4	ATGGCCCTTACGA	
E.colirrSE	1204 ATGGCCCTTACGACCCAGGGCTACACACCGTGTACAATGGCATATAGAATGAGACGCCATTAC	
Cam.jejunS	1183 ATGGCCCTTATGCCAGGGGACACACGTGTACAATGGCATATAGAATGAGACGCCATTAC	
Stp.aureus	1214 ATGGCCCTTATGTTGGCTACACACCGTGTACAATGGACAATACAAGGGAGGGAAACC	
E.colirrSE	1266 GCGAGAGGCAAGCGGACCTCATAAAGTGGCTGTAGTGGAGTCTGCAACTCGACTC	
Cam.jejunS	1245 GCGAGGCTGGAG-CAATCTATAAAATATGTCCTCAGTTCGGATTCTGCACACTCGAGAG	
Stp.aureus	1276 GCGAGGCTAACGCAAATCCATAAAGTGGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA	
E.colirrSE	1328 CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACCGTGAATACGTTGGGGC	
Cam.jejunS	1306 CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTGGGGT	
Stp.aureus	1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTGGGGT	
1743 (compl)	CGGTGAATACGTTGGGGC	

FIG. 89E

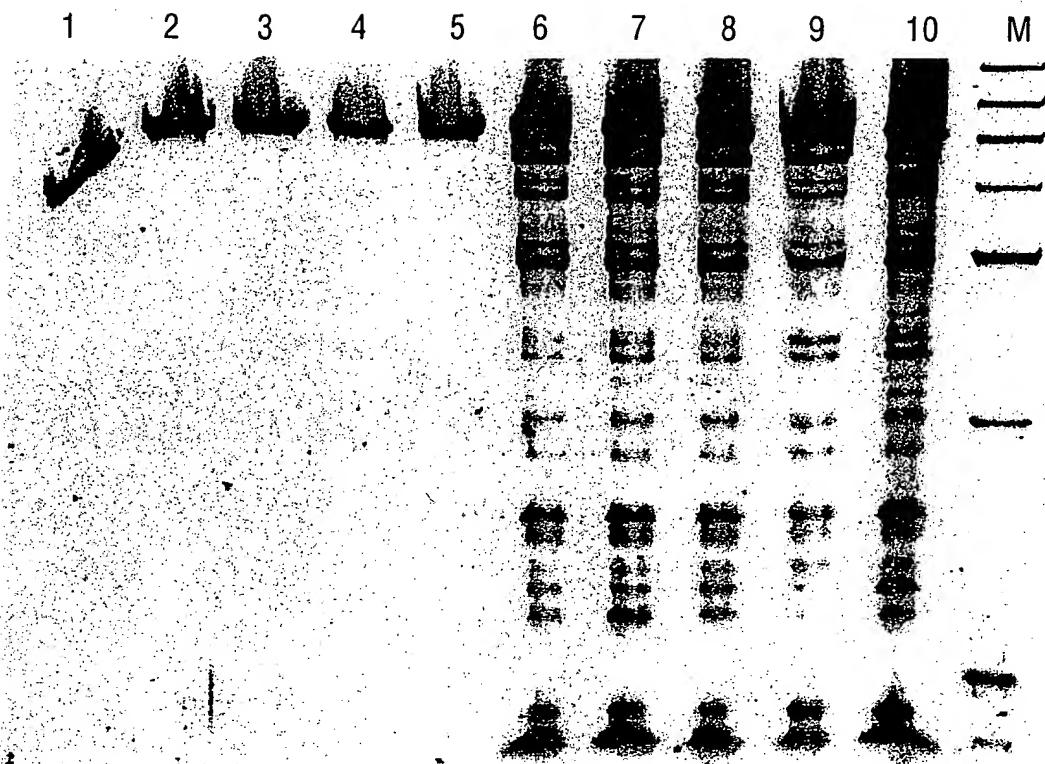
E. coli rrSE	1389	CTTGTACACACCGCCCCGTACACCATGGAGTTGATTCACTCGAAGCCGGAATACT- <u>-A-A</u>
Cam. jejun5	1368	CTTGTACTCACCGCCCCGTACACCATGGAGTTGATTCACTCGAAGCCGGAATACT- <u>-A-A</u>
Stp. aureus	1399	ATTGTACACACCGCCCCGTACACCATGGAGTTGTAACACCCGAAGCCGGTGGAGTAACCT
1743 (compl)		CTTGTAC
E. coli rrSE	1451	TCG=GGAGGGCGTACCACTTTGTATTCACTGGGTGAAGTCTCGTAACAAGGTAACCG
Cam. jejun5	1427	AC- <u>--T</u> -AGTTACCGTCCACAGTGGATCAGCGACTGGGTGAAGTCTGAACAAGGTAACCG
Stp. aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGACAATGATTGGGTGAAGTCTCGTAACAAGGTAACCT
E. coli rrSE	1512	TAGGGAACCTGGCGTGGATCACCTCTTA--
Cam. jejun5	1485	TAGGAGAACCTGGCGTGGATCACCTCT---
Stp. aureus	1523	TATCGGAAGGTGGGCTGGATCACCTCTTCT

FIG. 89F

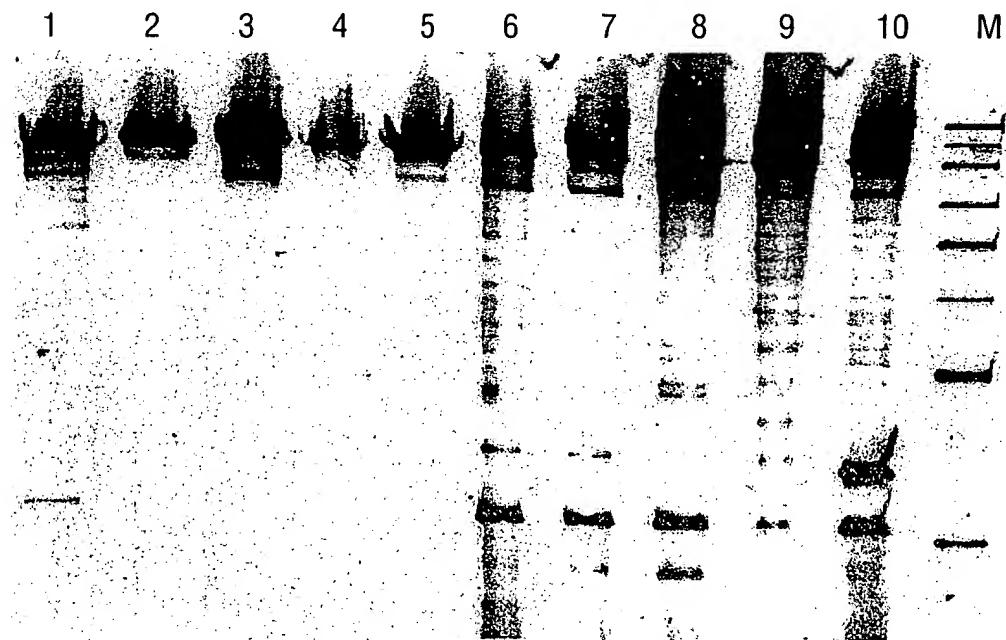
1 2 3 4 5 6 7 8



**FIG. 90**

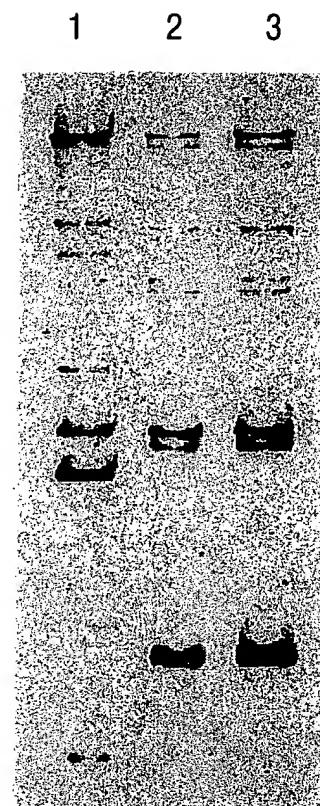


**FIG. 91A**

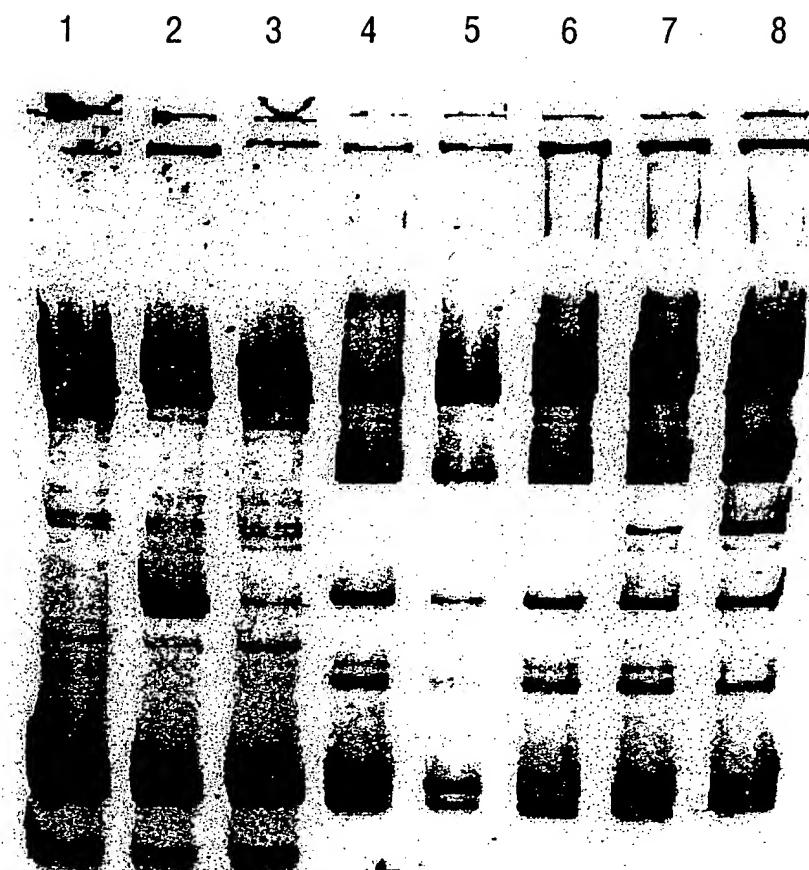


**FIG. 91B**

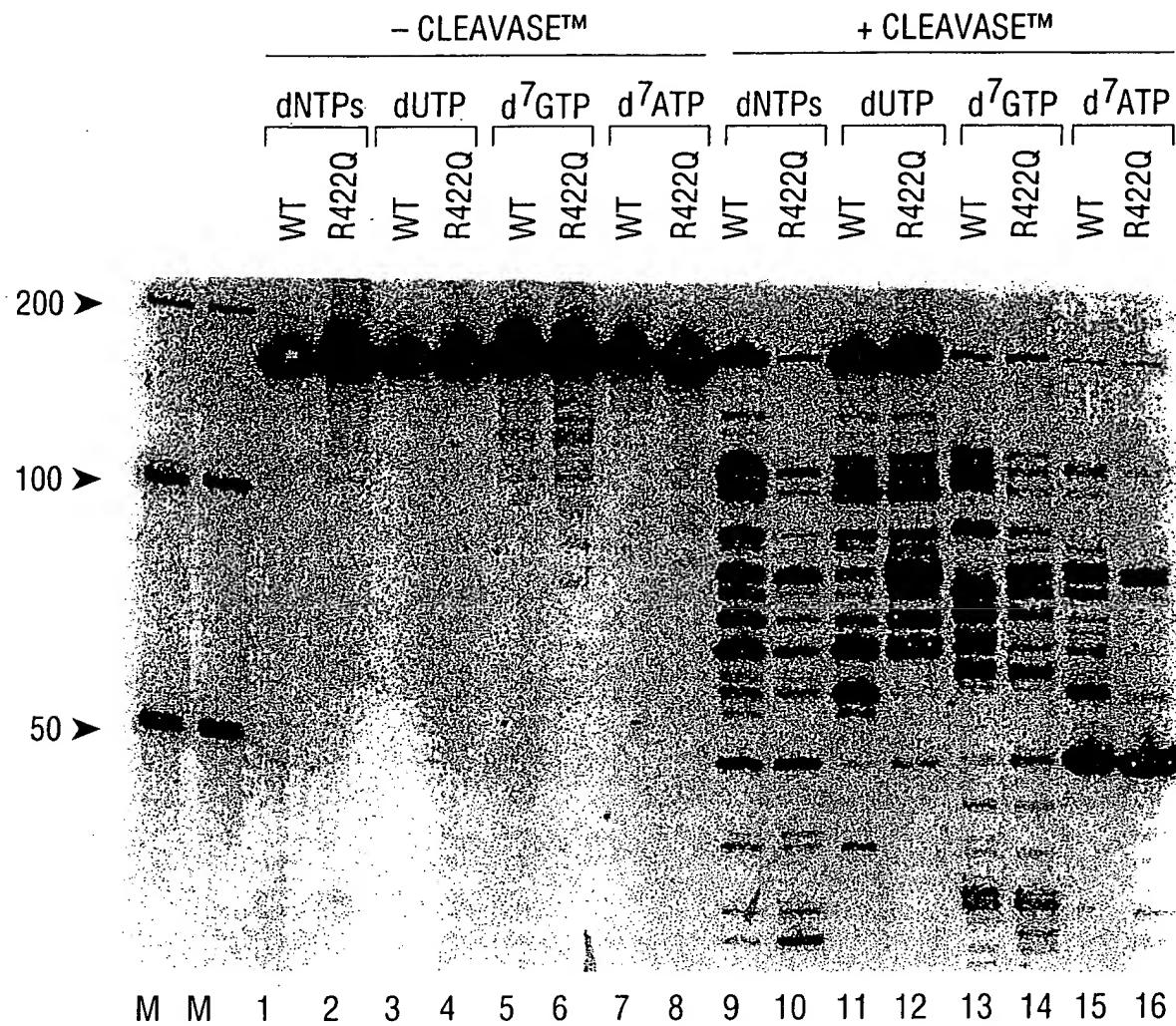
"Replacement Sheet"



**FIG. 92**



**FIG. 93**



**FIG. 94**

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